

# UTILITY PATENT APPLICATION TRANSMITTAL

(Only for new nonprovisional applications under 37 CFR 1.53(b))

Attorney Docket No.

GI 6069-74A

Total Pages

424

First Named Inventor or Application Identifier

Kenneth Jacobs et al.

## APPLICATION ELEMENTS

See MPEP chapter 600 concerning utility patent application contents.

ADDRESS TO: Assistant Commissioner for Patents  
Box Patent Application  
Washington, DC 20231

1. ☒ Fee Transmittal Form  
(Submit an original, and a duplicate for fee processing)

6. ☐ Microfiche Computer Program (Appendix)

2. ☒ Specification [Total Pages 295]

7. Nucleotide and/or Amino Acid Sequence Submission  
(If applicable, all necessary)

(preferred arrangement set forth below)

- Descriptive title of the invention
- Cross References to Related Applications
- Statement Regarding Fed sponsored R & D
- Reference to Microfiche Appendix
- Background of the Invention
- Brief Summary of the Invention
- Brief Description of the Drawings (if filed)
- Detailed Description
- Claim(s)
- Abstract of the Disclosure

a. ☒ Computer Readable Copy

b. ☒ Paper Copy (identical to computer copy) (127pp.)

c. ☒ Statement verifying identity of above copies

3. ☒ Drawing(s) (35 USC 113) [Total Sheets 2]

4. Oath or Declaration [Total Pages ]

a. ☐ Unsigned (original or copy)

b. ☐ Copy from a prior application (37 CFR 1.63(d))  
(for continuation/divisional with Box 17 completed)

[Note Box 5 below]

i. ☐ DELETION OF INVENTOR(S)  
Signed statement attached deleting  
inventor(s) named in the prior application,  
See 37 CFR 1.63(d)(2) and 1.33(b).

5. ☐ Incorporation By Reference (useable if Box 4b is checked)  
The entire disclosure of the prior application, from which  
a copy of the oath or declaration is supplied under Box  
4b, is considered as being part of the disclosure of the  
accompanying application and is hereby incorporated by  
reference therein.

## ACCOMPANYING APPLICATION PARTS

8. ☐ Assignment Papers (cover sheet & documents(s))

9. ☐ 37 CFR 3.73(b) Statement ☐ Power of Attorney  
(when there is an assignee)

10. ☐ English Translation Document (if applicable)

11. ☐ Information Disclosure  
Statement (IDS)/PTO-1449 ☐ Copies of IDS  
Citations

12. ☐ Preliminary Amendment

13. ☒ Return Receipt Postcard (MPEP 503)  
(Should be specifically itemized)

14. ☐ Small Entity ☐ Statement filed in prior application,  
Statement(s) Status still proper and desired

15. ☐ Certified Copy of Priority Document(s)  
(if foreign priority is claimed)

16. ☒ Other: ..Information Data Sheet.....

17. If a **CONTINUING APPLICATION**, check appropriate box and supply the requisite information: 60/084,564, 60/087,645, 60/093,712  
☐ Continuation ☐ Divisional ☒ Continuation-in-part (CIP) of prior application No.: 60/094,935, 60/095,880, 60/096,068

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## CERTIFICATE OF EXPRESS MAILING

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Typed or printed name Suzanne A. Sprunger, Ph.D.

Signature

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Date May 6, 1999

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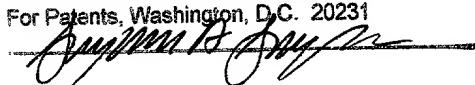
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#### Application Information

Title Line One ::  
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Formal Drawings ::  
Application Type ::  
Docket Number ::  
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Contract Number ::  
Grant Number ::  
Secrecy Order in Parent Application ::

SECRETED PROTEINS AND  
POLYNUCLEOTIDES ENCODING THEM  
2  
N  
Utility  
GI 6069-74A

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Registration Number Two :: 32,618  
Registration Number Three :: 32,245  
Registration Number Four :: 32,724

## Continuity Information

This application is a :: Continuation-in-Part of  
> Application One :: 60/084,564  
Filing Date :: May 7, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Two :: 60/087,645  
Filing Date :: June 2, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Three :: 60/093,712  
Filing Date :: July 22, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Four :: 60/094,935  
Filing Date :: July 31, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application Five :: 60/095,880  
Filing Date :: August 10, 1998  
Patent Number ::  
This application is a :: Continuation-in-Part of  
> Application One :: 60/096,068  
Filing Date :: August 11, 1998  
Patent Number ::

## Prior Foreign Applications

Foreign Application One ::  
Filing Date ::  
Country ::  
Priority Claimed ::

SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM

- 5 This application is a continuation-in-part of the following applications:
- (1) provisional application Ser. No. 60/084,564, filed May 7, 1998;
  - (2) provisional application Ser. No. 60/087,645, filed June 2, 1998;
  - (3) provisional application Ser. No. 60/093,712, filed July 22, 1998;
  - (4) provisional application Ser. No. 60/094,935, filed July 31, 1998;
  - 10 (5) provisional application Ser. No. 60/095,880, filed August 10, 1998;
  - (6) provisional application Ser. No. 60/096,068, filed August 11, 1998;
- all of which are incorporated by reference herein.

FIELD OF THE INVENTION

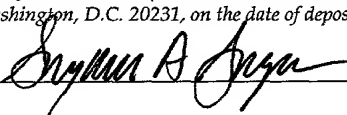
- 15 The present invention provides novel polynucleotides and proteins encoded by such polynucleotides, along with therapeutic, diagnostic and research utilities for these polynucleotides and proteins.

BACKGROUND OF THE INVENTION

- 20 Technology aimed at the discovery of protein factors (including e.g., cytokines, such as lymphokines, interferons, CSFs and interleukins) has matured rapidly over the past decade. The now routine hybridization cloning and expression cloning techniques clone novel polynucleotides "directly" in the sense that they rely on information directly related to the discovered protein (i.e., partial DNA/amino acid sequence of the protein
- 25 in the case of hybridization cloning; activity of the protein in the case of expression cloning). More recent "indirect" cloning techniques such as signal sequence cloning, which isolates DNA sequences based on the presence of a now well-recognized secretory leader sequence motif, as well as various PCR-based or low stringency hybridization cloning techniques, have advanced the state of the art by making available large numbers of
- 30 DNA/amino acid sequences for proteins that are known to have biological activity by virtue of their secreted nature in the case of leader sequence cloning, or by virtue of the cell or tissue source in the case of PCR-based techniques. It is to these proteins and the polynucleotides encoding them that the present invention is directed.

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0930611-050699

## SUMMARY OF THE INVENTION

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession  
10 number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:2;
- 20 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:2;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 25 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:1.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366; the nucleotide sequence of the full-length protein coding sequence of clone bn365\_53 deposited under accession number ATCC

98752; or the nucleotide sequence of a mature protein coding sequence of clone bn365\_53 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752. In further preferred  
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having  
10 biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:1.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and

(ab) the nucleotide sequence of the cDNA insert of clone bn365\_53 deposited under accession number ATCC 98752;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

30 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1; and



(bb) the nucleotide sequence of the cDNA insert of clone

bn365\_53 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:1 to  
10 a nucleotide sequence corresponding to the 3' end of SEQ ID NO:1, but excluding the poly(A) tail at the 3' end of SEQ ID NO:1. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of  
15 SEQ ID NO:1 from nucleotide 61 to nucleotide 366, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:1 from nucleotide 61 to nucleotide 366.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:2;

(b) a fragment of the amino acid sequence of SEQ ID NO:2, the fragment comprising eight contiguous amino acids of SEQ ID NO:2; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
25 bn365\_53 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:2. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:2, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:2 having biological activity, the fragment comprising the amino acid sequence from amino acid 46 to amino acid 55 of SEQ ID NO:2.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;
- (h) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:4;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:4;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:3.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915; the nucleotide sequence of SEQ ID NO:3

from nucleotide 1358 to nucleotide 1915; the nucleotide sequence of the full-length protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone bo342\_2 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:3.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(ab) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3; and

(bb) the nucleotide sequence of the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:3 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:3, but excluding the poly(A) tail at the 3' end of SEQ ID NO:3. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the

15 cDNA sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 206 to nucleotide 1915. Also preferably the polynucleotide isolated according to the above

20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:3 from nucleotide 1358 to nucleotide 1915.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:4;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:4, the fragment comprising eight contiguous amino acids of SEQ ID NO:4; and

(c) the amino acid sequence encoded by the cDNA insert of clone bo342\_2 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:4. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:4, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:4 having biological activity, the fragment comprising the amino acid sequence from amino acid 280 to amino acid 289 of SEQ ID NO:4.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:6;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:6;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:5.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689; the nucleotide sequence of the full-length protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn721\_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:5.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(ab) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5; and

(bb) the nucleotide sequence of the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5, and extending  
15 contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:5 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:5, but excluding the poly(A) tail at the 3' end of SEQ ID NO:5. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, and extending  
20 contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:5 from nucleotide 749 to nucleotide 2689.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:6;

(b) a fragment of the amino acid sequence of SEQ ID NO:6, the fragment comprising eight contiguous amino acids of SEQ ID NO:6; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone dn721\_8 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:6. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:6 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:6, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:6 having biological activity, the fragment comprising the amino acid sequence from amino acid 318 to amino acid 327 of SEQ ID NO:6.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:8;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:8;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and



(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:7.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484; the nucleotide sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892; the nucleotide sequence of the full-length protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone dn834\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:8, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:7.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and

(ab) the nucleotide sequence of the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7; and
    - (bb) the nucleotide sequence of the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;
  - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:7 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:7, but excluding the poly(A) tail at the 3' end of SEQ ID NO:7. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 20 to nucleotide 484. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:7 from nucleotide 18 to nucleotide 892.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:8;

(b) a fragment of the amino acid sequence of SEQ ID NO:8, the fragment comprising eight contiguous amino acids of SEQ ID NO:8; and

(c) the amino acid sequence encoded by the cDNA insert of clone dn834\_1 deposited under accession number ATCC 98752;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:8. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:8, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:8 having biological activity, the fragment comprising the amino acid sequence from amino acid 72 to amino acid 81 of SEQ ID NO:8.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:10;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:10;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:9.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420; the nucleotide sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420; the nucleotide sequence of the full-length protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pd278\_5 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:10, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:9.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(ab) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9; and

(bb) the nucleotide sequence of the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:9 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:9, but excluding the poly(A) tail at the 3' end of SEQ ID NO:9. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 803 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 803 to

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nucleotide 1420. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:9 from nucleotide 1022 to nucleotide 1420.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:10;
- (b) a fragment of the amino acid sequence of SEQ ID NO:10, the fragment comprising eight contiguous amino acids of SEQ ID NO:10; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pd278\_5 deposited under accession number ATCC 98752;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:10. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:10, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:10 having biological activity, the fragment comprising the amino acid sequence from amino acid 98 to amino acid 107 of SEQ ID NO:10.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number
- 30 ATCC 98752;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:12;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:12;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:11.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295; the nucleotide sequence of the full-length protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pe80\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:12, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:11.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:11, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:11; and
- (ab) the nucleotide sequence of the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 pe80\_1 deposited under accession number ATCC 98752;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:11 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:11, but excluding the poly(A) tail at the 3' end of SEQ ID NO:11. Also preferably the



polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:11 from nucleotide 918 to nucleotide 1295.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:12;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:12, the fragment comprising eight contiguous amino acids of SEQ ID NO:12; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pe80\_1 deposited under accession number ATCC 98752;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:12. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:12, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:12 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:12.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:13 from nucleotide 348 to nucleotide 428;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:14;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:14;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:13.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428; the nucleotide sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428; the nucleotide sequence of the full-length protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm113\_1 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having

biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:13.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10

(aa) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(ab) the nucleotide sequence of the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

15

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25

(ba) SEQ ID NO:13, but excluding the poly(A) tail at the 3' end of SEQ ID NO:13; and

(bb) the nucleotide sequence of the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:13 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:13 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:13. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 189 to nucleotide 428. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:13 from nucleotide 348 to nucleotide 428.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:14;
- (b) a fragment of the amino acid sequence of SEQ ID NO:14, the fragment comprising eight contiguous amino acids of SEQ ID NO:14; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone pm113\_1 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:14. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:14, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:14 having biological activity, the fragment comprising the amino acid sequence from amino acid 35 to amino acid 44 of SEQ ID NO:14.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:16;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:16;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:15.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496; the nucleotide sequence of the full-length protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pm749\_8 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:15.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(ab) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15; and

(bb) the nucleotide sequence of the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:15 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:15, but excluding the poly(A) tail at the 3' end of SEQ ID NO:15. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:15 from nucleotide 108 to nucleotide 1496.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:16;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:16, the fragment comprising eight contiguous amino acids of SEQ ID NO:16; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pm749\_8 deposited under accession number ATCC 98752;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:16. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:16, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:16 having biological activity, the fragment comprising the amino acid sequence from amino acid 226 to amino acid 235 of SEQ ID NO:16.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:18;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:18;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:17.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023; the nucleotide sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023; the nucleotide sequence of the full-length protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pt31\_4 deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752. In further preferred embodiments, the



present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a polynucleotide encoding a protein comprising a  
5 fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:17.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(ab) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (ba) SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17; and

(bb) the nucleotide sequence of the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:17 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:17, but excluding the poly(A) tail at the 3' end of SEQ ID NO:17. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide  
10 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 44 to nucleotide 2023. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:17 from nucleotide 137 to nucleotide 2023, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:17 from nucleotide 137 to nucleotide 2023.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:18;
- (b) a fragment of the amino acid sequence of SEQ ID NO:18, the fragment comprising eight contiguous amino acids of SEQ ID NO:18; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone pt31\_4 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:18. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:18, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:18 having biological activity, the fragment comprising the amino acid sequence from amino acid 325 to amino acid 334 of SEQ ID NO:18.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:20;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:20;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:19.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299; the nucleotide sequence of the full-length protein coding sequence of clone pv296\_5 deposited under accession number ATCC 98752; or the nucleotide sequence of a mature protein coding sequence of clone pv296\_5

deposited under accession number ATCC 98752. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:19.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and
    - (ab) the nucleotide sequence of the cDNA insert of clone pv296\_5 deposited under accession number ATCC 98752;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19; and

(bb) the nucleotide sequence of the cDNA insert of clone

pv296\_5 deposited under accession number ATCC 98752;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:19 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:19, but excluding the poly(A) tail at the 3' end of SEQ ID NO:19. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:19 from nucleotide 24 to nucleotide 299.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:20;

(b) a fragment of the amino acid sequence of SEQ ID NO:20, the fragment comprising eight contiguous amino acids of SEQ ID NO:20; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
25 pv296\_5 deposited under accession number ATCC 98752;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:20. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:20, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:20 having biological activity, the fragment comprising the amino acid sequence from amino acid 41 to amino acid 50 of SEQ ID NO:20.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- 10 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
- 15 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
- 20 (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- 25 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least
- 30 25% of the length of SEQ ID NO:21.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008; the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone er311\_20

deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:21.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and
    - (ab) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21; and

(bb) the nucleotide sequence of the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:21 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:21, but excluding the poly(A) tail at the 3' end of SEQ ID NO:21. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
20 consisting of:

(a) the amino acid sequence of SEQ ID NO:22;

(b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and

(c) the amino acid sequence encoded by the cDNA insert of clone  
25 er311\_20 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:22. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment preferably  
30 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:22, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22 having biological activity, the fragment comprising the amino acid sequence from amino acid 328 to amino acid 337 of SEQ ID NO:22.



In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:24;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:24;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:23.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043; the nucleotide sequence of SEQ ID NO:23

from nucleotide 919 to nucleotide 2043; the nucleotide sequence of the full-length protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone fh149\_12 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:23.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(ab) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23; and

(bb) the nucleotide sequence of the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:23 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:23, but excluding the poly(A) tail at the 3' end of SEQ ID NO:23. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 484 to nucleotide 2043. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:23 from nucleotide 919 to nucleotide 2043.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:24;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:24, the fragment comprising eight contiguous amino acids of SEQ ID NO:24; and

(c) the amino acid sequence encoded by the cDNA insert of clone fh149\_12 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:24. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:24, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:24 having biological activity, the fragment comprising the amino acid sequence from amino acid 255 to amino acid 264 of SEQ ID NO:24.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:26;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:26;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:25.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099; the nucleotide sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099; the nucleotide sequence of the full-length protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pc201\_6 deposited under accession number ATCC 98781. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:25.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

(ab) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:25, but excluding the poly(A) tail at the 3' end of SEQ ID NO:25; and

10 (bb) the nucleotide sequence of the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:25 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:25, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:25. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 47 to nucleotide 1099. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:25 from  
30 nucleotide 143 to nucleotide 1099, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:25 from nucleotide 143 to nucleotide 1099.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:26;
- (b) a fragment of the amino acid sequence of SEQ ID NO:26, the fragment comprising eight contiguous amino acids of SEQ ID NO:26; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pc201\_6 deposited under accession number ATCC 98781;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:26. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:26, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:26 having biological activity, the fragment comprising the amino acid sequence from amino acid 170 to amino acid 179 of SEQ ID NO:26.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:28;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:28;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:27.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259; the nucleotide sequence of the full-length protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pl87\_1 deposited under accession number ATCC 98781. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:28, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:27.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
30 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and



(ab) the nucleotide sequence of the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27; and

15 (bb) the nucleotide sequence of the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:27 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:27, but excluding the poly(A) tail at the 3' end of SEQ ID NO:27. Also preferably the  
25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:27 from nucleotide 5 to nucleotide 259, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:27 from nucleotide  
30 5 to nucleotide 259.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:28;

(b) a fragment of the amino acid sequence of SEQ ID NO:28, the fragment comprising eight contiguous amino acids of SEQ ID NO:28; and

(c) the amino acid sequence encoded by the cDNA insert of clone pl87\_1 deposited under accession number ATCC 98781;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:28. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:28, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:28 having biological activity, the fragment comprising the amino acid sequence from amino acid 37 to amino acid 46 of SEQ ID NO:28.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284;

20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:30;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:30;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:29.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284; the nucleotide sequence of the full-length protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781; or the nucleotide sequence of a mature protein coding sequence of clone pm514\_4 deposited under accession number ATCC 98781. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:30, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:29.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

(ab) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

5 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

10 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29; and

15 (bb) the nucleotide sequence of the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:29 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:29, but excluding the poly(A) tail at the 3' end of SEQ ID NO:29. Also preferably the  
25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:29 from nucleotide 62 to nucleotide 2284, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:29 from nucleotide  
30 62 to nucleotide 2284.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:30;

(b) a fragment of the amino acid sequence of SEQ ID NO:30, the fragment comprising eight contiguous amino acids of SEQ ID NO:30; and

(c) the amino acid sequence encoded by the cDNA insert of clone pm514\_4 deposited under accession number ATCC 98781;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:30. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:30, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:30 having biological activity, the fragment comprising the amino acid sequence from amino acid 365 to amino acid 374 of SEQ ID NO:30.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:32;

- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:32;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:31.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997; the nucleotide sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997; the nucleotide sequence of the full-length protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone co155\_12 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:32, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:31.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(ab) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31; and

(bb) the nucleotide sequence of the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:31 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:31, but excluding the poly(A) tail at the 3' end of SEQ ID NO:31. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 36 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide

36 to nucleotide 1997. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:31 from nucleotide 135 to nucleotide 1997.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:32;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:32, the fragment comprising eight contiguous amino acids of SEQ ID NO:32; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone co155\_12 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:32. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:32, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:32 having biological activity, the fragment comprising the amino acid sequence from amino acid 322 to amino acid 331 of SEQ ID NO:32.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:33 from nucleotide 84 to nucleotide 1343;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:34;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:34;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:33.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343; the nucleotide sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343; the nucleotide sequence of the full-length protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone fn189\_13 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having

biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:33.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(ab) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:33, but excluding the poly(A) tail at the 3' end of SEQ ID NO:33; and

(bb) the nucleotide sequence of the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

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ID NO:33 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:33 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:33. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 5 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 21 to nucleotide 1343. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID 10 NO:33 from nucleotide 84 to nucleotide 1343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:33 from nucleotide 84 to nucleotide 1343.

In other embodiments, the present invention provides a composition comprising 15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:34;
- (b) a fragment of the amino acid sequence of SEQ ID NO:34, the fragment comprising eight contiguous amino acids of SEQ ID NO:34; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone fn189\_13 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:34. In further preferred 25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:34, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:34 having biological activity, the fragment comprising the amino acid sequence from amino acid 215 to amino acid 224 of SEQ ID NO:34.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:35;



encodes the full-length or a mature protein encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:36, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:36 having biological activity, the fragment comprising the amino acid sequence from amino acid 77 to amino acid 86 of SEQ ID NO:36.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:35.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (aa) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

- (ab) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

- (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- (ba) SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35; and

(bb) the nucleotide sequence of the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ  
10 ID NO:35 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:35, but excluding the poly(A) tail at the 3' end of SEQ ID NO:35. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
15 of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 66 to nucleotide 557. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, and extending contiguously from a  
20 nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:35 from nucleotide 235 to nucleotide 899.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group  
25 consisting of:

(a) the amino acid sequence of SEQ ID NO:36;

(b) the amino acid sequence of SEQ ID NO:36 from amino acid 58 to amino acid 164;

(c) a fragment of the amino acid sequence of SEQ ID NO:36, the  
30 fragment comprising eight contiguous amino acids of SEQ ID NO:36; and

(d) the amino acid sequence encoded by the cDNA insert of clone lv2\_47 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:36 or the amino acid sequence

of SEQ ID NO:36 from amino acid 58 to amino acid 164. In further preferred  
embodiments, the present invention provides a protein comprising a fragment of the  
amino acid sequence of SEQ ID NO:36 having biological activity, the fragment preferably  
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
5 of SEQ ID NO:36, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:36 having biological activity, the fragment comprising the amino acid sequence  
from amino acid 77 to amino acid 86 of SEQ ID NO:36.

In one embodiment, the present invention provides a composition comprising an  
isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:37;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:37 from nucleotide 104 to nucleotide 499;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
15 NO:37 from nucleotide 215 to nucleotide 499;
- (d) a polynucleotide comprising the nucleotide sequence of the full-  
length protein coding sequence of clone ml243\_1 deposited under accession  
number ATCC 98808;
- (e) a polynucleotide encoding the full-length protein encoded by the  
20 cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
protein coding sequence of clone ml243\_1 deposited under accession number  
ATCC 98808;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
25 insert of clone ml243\_1 deposited under accession number ATCC 98808;
- (h) a polynucleotide encoding a protein comprising the amino acid  
sequence of SEQ ID NO:38;
- (i) a polynucleotide encoding a protein comprising a fragment of the  
amino acid sequence of SEQ ID NO:38 having biological activity, the fragment  
30 comprising eight contiguous amino acids of SEQ ID NO:38;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
(a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein  
of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:37.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499; the nucleotide sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499; the nucleotide sequence of the full-length protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone ml243\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:37.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

(ab) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and



(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:37, but excluding the poly(A) tail at the 3' end of SEQ ID NO:37; and

10 (bb) the nucleotide sequence of the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:37 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:37, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:37. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 104 to nucleotide 499. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:37 from  
30 nucleotide 215 to nucleotide 499, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:37 from nucleotide 215 to nucleotide 499.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:38;
- (b) a fragment of the amino acid sequence of SEQ ID NO:38, the fragment comprising eight contiguous amino acids of SEQ ID NO:38; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml243\_1 deposited under accession number ATCC 98808;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:38. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment preferably  
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:38, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:38 having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:38.

In one embodiment, the present invention provides a composition comprising an  
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861;
- 20 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- 25 (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
- 30 (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:40;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:40;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

5 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:39.

10 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861; the nucleotide sequence of the full-length protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pm96\_9 deposited under accession number ATCC 98808. In other preferred embodiments, the  
15 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most  
20 preferably thirty) contiguous amino acids of SEQ ID NO:40, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ  
25 ID NO:39.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

30 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and

- (ab) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 5 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that
    - 10 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
      - (ba) SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39; and
      - (bb) the nucleotide sequence of the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;
      - 15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
      - (iii) amplifying human DNA sequences; and
      - (iv) isolating the polynucleotide products of step (b)(iii).
  - 20 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:39 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:39, but excluding the poly(A) tail at the 3' end of SEQ ID NO:39. Also preferably the
  - 25 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:39 from nucleotide 2172 to nucleotide 2861, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:39 from nucleotide
  - 30 2172 to nucleotide 2861.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:40;

(b) a fragment of the amino acid sequence of SEQ ID NO:40, the fragment comprising eight contiguous amino acids of SEQ ID NO:40; and

(c) the amino acid sequence encoded by the cDNA insert of clone pm96\_9 deposited under accession number ATCC 98808;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:40. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:40, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:40 having biological activity, the fragment comprising the amino acid sequence from amino acid 110 to amino acid 119 of SEQ ID NO:40.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:42;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:42;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:41.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762; the nucleotide sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762; the nucleotide sequence of the full-length protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pu261\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:42, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:41.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(ab) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41; and

(bb) the nucleotide sequence of the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:41 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:41, but excluding the poly(A) tail at the 3' end of SEQ ID NO:41. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 43 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide

43 to nucleotide 762. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:41 from nucleotide 427 to nucleotide 762.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:42;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:42, the fragment comprising eight contiguous amino acids of SEQ ID NO:42; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pu261\_1 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:42. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:42, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:42 having biological activity, the fragment comprising the amino acid sequence from amino acid 115 to amino acid 124 of SEQ ID NO:42.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;



(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:44;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:44;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:43.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824; the nucleotide sequence of the full-length protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone pw214\_15 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:44, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:43.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (ab) the nucleotide sequence of the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 pw214\_15 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:43 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:43, but excluding the poly(A) tail at the 3' end of SEQ ID NO:43. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824, to a nucleotide  
5 sequence corresponding to the 3' end of said sequence of SEQ ID NO:43 from nucleotide 579 to nucleotide 824.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:44;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:44, the fragment comprising eight contiguous amino acids of SEQ ID NO:44; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone pw214\_15 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:44. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
20 of SEQ ID NO:44, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:44 having biological activity, the fragment comprising the amino acid sequence from amino acid 36 to amino acid 45 of SEQ ID NO:44.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession  
30 number ATCC 98808;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:46;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:46;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:45.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383; the nucleotide sequence of the full-length protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qb56\_19 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:46, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:45.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 10 (aa) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (ab) the nucleotide sequence of the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 qb56\_19 deposited under accession number ATCC 98808;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:45 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:45, but excluding the poly(A) tail at the 3' end of SEQ ID NO:45. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:45 from nucleotide 6 to nucleotide 383.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:46;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:46, the fragment comprising eight contiguous amino acids of SEQ ID NO:46; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qb56\_19 deposited under accession number ATCC 98808;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:46. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:46, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:46 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:46.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:47 from nucleotide 242 to nucleotide 1273;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:48;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:48;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:47.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273; the nucleotide sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273; the nucleotide sequence of the full-length protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qc646\_1 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having

biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:47.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(ab) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:47, but excluding the poly(A) tail at the 3' end of SEQ ID NO:47; and

(bb) the nucleotide sequence of the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



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ID NO:47 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:47 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:47. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 170 to nucleotide 1273. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:47 from nucleotide 242 to nucleotide 1273.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:48;
- (b) a fragment of the amino acid sequence of SEQ ID NO:48, the fragment comprising eight contiguous amino acids of SEQ ID NO:48; and
- (c) the amino acid sequence encoded by the cDNA insert of clone qc646\_1 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:48. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:48, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:48 having biological activity, the fragment comprising the amino acid sequence from amino acid 179 to amino acid 188 of SEQ ID NO:48.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:50;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:50;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:49.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097; the nucleotide sequence of the full-length protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf116\_2 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:49.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(ab) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49; and

(bb) the nucleotide sequence of the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:49 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:49, but excluding the poly(A) tail at the 3' end of SEQ ID NO:49. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:49 from nucleotide 183 to nucleotide 1097.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:50;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:50, the fragment comprising eight contiguous amino acids of SEQ ID NO:50; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone qf116\_2 deposited under accession number ATCC 98808;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:50. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:50, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:50 having biological activity, the fragment comprising the amino acid sequence from amino acid 147 to amino acid 156 of SEQ ID NO:50.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:52;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:52;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:51.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741; the nucleotide sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741; the nucleotide sequence of the full-length protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808; or the nucleotide sequence of a mature protein coding sequence of clone qf662\_3 deposited under accession number ATCC 98808. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a polynucleotide encoding  
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:51.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize  
15 in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:51, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:51; and

(ab) the nucleotide sequence of the cDNA insert of clone  
qf662\_3 deposited under accession number ATCC 98808;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the  
probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that  
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from  
the group consisting of:

(ba) SEQ ID NO:51, but excluding the poly(A) tail at the  
30 3' end of SEQ ID NO:51; and

(bb) the nucleotide sequence of the cDNA insert of clone  
qf662\_3 deposited under accession number ATCC 98808;

(ii) hybridizing said primer(s) to human genomic DNA in  
conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:51 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:51, but excluding the poly(A) tail at the 3' end of SEQ ID NO:51. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide  
10 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 160 to nucleotide 741. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:51 from nucleotide 595 to nucleotide 741, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:51 from nucleotide 595 to nucleotide 741.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:52;
- (b) a fragment of the amino acid sequence of SEQ ID NO:52, the fragment comprising eight contiguous amino acids of SEQ ID NO:52; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone qf662\_3 deposited under accession number ATCC 98808;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:52. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:52, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:52 having biological activity, the fragment comprising the amino acid sequence from amino acid 92 to amino acid 101 of SEQ ID NO:52.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:54;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:54;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:53.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196; the nucleotide sequence of SEQ ID NO:53



from nucleotide 1002 to nucleotide 1196; the nucleotide sequence of the full-length protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone am748\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:53.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(ab) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53; and

(bb) the nucleotide sequence of the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:53 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:53, but excluding the poly(A) tail at the 3' end of SEQ ID NO:53. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 924 to nucleotide 1196. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:53 from nucleotide 1002 to nucleotide 1196.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:54;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:54, the fragment comprising eight contiguous amino acids of SEQ ID NO:54; and

(c) the amino acid sequence encoded by the cDNA insert of clone am748\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:54. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:54, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:54 having biological activity, the fragment comprising the amino acid sequence from amino acid 40 to amino acid 49 of SEQ ID NO:54.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310;
- 15 (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817;
- 20 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:56;
- 25 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:56;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- 30 (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:55.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310; the nucleotide sequence of the full-length protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cj507\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:55.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(ab) the nucleotide sequence of the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55; and

(bb) the nucleotide sequence of the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:55 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:55, but excluding the poly(A) tail at the 3' end of SEQ ID NO:55. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide  
20 1310, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:55 from nucleotide 51 to nucleotide 1310.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:56;

(b) a fragment of the amino acid sequence of SEQ ID NO:56, the fragment comprising eight contiguous amino acids of SEQ ID NO:56; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cj507\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:56. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:56 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:56, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:56 having biological activity, the fragment comprising the amino acid sequence from amino acid 205 to amino acid 214 of SEQ ID NO:56.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:58;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:58;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:57.

5 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328; the nucleotide sequence of the full-length protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cn922\_5 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert  
10 of clone cn922\_5 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a polynucleotide encoding  
15 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:57.

20 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
25 consisting of:

(aa) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(ab) the nucleotide sequence of the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

30 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57; and

(bb) the nucleotide sequence of the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:57 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:57, but excluding the poly(A) tail at the 3' end of SEQ ID NO:57. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide  
20 1328, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:57 from nucleotide 195 to nucleotide 1328.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:58;

(b) a fragment of the amino acid sequence of SEQ ID NO:58, the fragment comprising eight contiguous amino acids of SEQ ID NO:58; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cn922\_5 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:58. In further preferred embodiments, the present invention provides a protein comprising a fragment of the



amino acid sequence of SEQ ID NO:58 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:58, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:58 having biological activity, the fragment comprising the amino acid sequence from amino acid 184 to amino acid 193 of SEQ ID NO:58.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817;

(d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:60;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:60;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:59.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942; the nucleotide sequence of the full-length protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw691\_11 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence from amino acid 139 to amino acid 148 of SEQ ID NO:60.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:59.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(ab) the nucleotide sequence of the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (ba) SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59; and

(bb) the nucleotide sequence of the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

10 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59, and  
15 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:59 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:59, but excluding the poly(A) tail at the 3' end of SEQ ID NO:59. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide  
20 942, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:59 from nucleotide 76 to nucleotide 942.

In other embodiments, the present invention provides a composition comprising  
25 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:60;

(b) a fragment of the amino acid sequence of SEQ ID NO:60, the fragment comprising eight contiguous amino acids of SEQ ID NO:60; and

30 (c) the amino acid sequence encoded by the cDNA insert of clone cw691\_11 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:60. In further preferred embodiments, the present invention provides a protein comprising a fragment of the

amino acid sequence of SEQ ID NO:60 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:60, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:60 having biological activity, the fragment comprising the amino acid sequence  
5 from amino acid 139 to amino acid 148 of SEQ ID NO:60.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61;
- 10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession  
15 number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature  
20 protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid  
25 sequence of SEQ ID NO:62;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:62;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of  
30 (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:61.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252; the nucleotide sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252; the nucleotide sequence of the full-length protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1000\_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:62, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:61.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:61 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:61, but excluding the poly(A) tail at the 3' end of SEQ ID NO:61. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 11 to nucleotide 1252. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:61 from nucleotide 119 to nucleotide 1252.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:62;

(b) a fragment of the amino acid sequence of SEQ ID NO:62, the fragment comprising eight contiguous amino acids of SEQ ID NO:62; and

(c) the amino acid sequence encoded by the cDNA insert of clone cw1000\_2 deposited under accession number ATCC 98817;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:62. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:62, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:62 having biological activity, the fragment comprising the amino acid sequence from amino acid 202 to amino acid 211 of SEQ ID NO:62.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:64;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:64;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:63.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296; the nucleotide sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296; the nucleotide sequence of the full-length protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone cw1640\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:64, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:63.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:



(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:63 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:63, but excluding the poly(A) tail at the 3' end of SEQ ID NO:63. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 46 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide

46 to nucleotide 1296. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:63 from nucleotide 451 to nucleotide 1296.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:64;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:64, the fragment comprising eight contiguous amino acids of SEQ ID NO:64; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cw1640\_1 deposited under accession number ATCC 98817;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:64. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:64, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:64 having biological activity, the fragment comprising the amino acid sequence from amino acid 203 to amino acid 212 of SEQ ID NO:64.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:65 from nucleotide 474 to nucleotide 827;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:66;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:65.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827; the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827; the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the

fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:65.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(ab) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:65, but excluding the poly(A) tail at the 3' end of SEQ ID NO:65; and

(bb) the nucleotide sequence of the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

5 ID NO:65 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:65 , but excluding the poly(A) tail at the 3' end of SEQ ID NO:65. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:66. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:66, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66 having biological activity, the fragment comprising the amino acid sequence from amino acid 122 to amino acid 131 of SEQ ID NO:66.

30 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:68;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:68;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:67.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529; the nucleotide sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529; the nucleotide sequence of the full-length protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone dd426\_1 deposited under accession number ATCC 98817. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:68.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:67.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67; and
    - (bb) the nucleotide sequence of the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:67 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:67, but excluding the poly(A) tail at the 3' end of SEQ ID NO:67. Also preferably the  
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 149 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:67 from nucleotide  
15 149 to nucleotide 529. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529, to a nucleotide sequence corresponding to the 3' end of  
20 said sequence of SEQ ID NO:67 from nucleotide 413 to nucleotide 529.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:68;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:68, the fragment comprising eight contiguous amino acids of SEQ ID NO:68; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dd426\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such  
30 protein comprises the amino acid sequence of SEQ ID NO:68. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:68 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:68, or a protein comprising a fragment of the amino acid sequence of SEQ



ID NO:68 having biological activity, the fragment comprising the amino acid sequence from amino acid 58 to amino acid 67 of SEQ ID NO:68.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:69 from nucleotide 88 to nucleotide 543;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (e) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone di393\_2 deposited under accession number ATCC 98817;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:70;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment  
25 comprising eight contiguous amino acids of SEQ ID NO:70;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:69.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543; the nucleotide sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543; the nucleotide sequence of the full-length protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817; or the nucleotide sequence of a mature protein coding sequence of clone di393\_2 deposited under accession number ATCC 98817. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment comprising the amino acid sequence from amino acid 80 to amino acid 89 of SEQ ID NO:70.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:69.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and
    - (ab) the nucleotide sequence of the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69; and

(bb) the nucleotide sequence of the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:69 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:69, but excluding the poly(A) tail at the 3' end of SEQ ID NO:69. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 31 to nucleotide 543. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:69 from nucleotide 88 to nucleotide 543.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:70;

(b) a fragment of the amino acid sequence of SEQ ID NO:70, the fragment comprising eight contiguous amino acids of SEQ ID NO:70; and

(c) the amino acid sequence encoded by the cDNA insert of clone di393\_2 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:70. In further preferred  
5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:70 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:70, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:70 having biological activity, the fragment comprising the amino acid sequence  
10 from amino acid 80 to amino acid 89 of SEQ ID NO:70.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71;

15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;

20 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818;

25 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:72;

(h) a polynucleotide encoding a protein comprising a fragment of the  
30 amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:72;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

5 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:71.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356; the nucleotide sequence of the full-length  
10 protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dj167\_2 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818. In further preferred  
15 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having  
20 biological activity, the fragment comprising the amino acid sequence from amino acid 195 to amino acid 204 of SEQ ID NO:72.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:71.

Further embodiments of the invention provide isolated polynucleotides produced  
25 according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

30 (aa) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and  
(ab) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);

5 and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (ba) SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71; and

(bb) the nucleotide sequence of the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818;

15 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71, and  
20 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:71 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:71, but excluding the poly(A) tail at the 3' end of SEQ ID NO:71. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:71 from nucleotide  
25 1356, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:71 from nucleotide 157 to nucleotide 1356.

In other embodiments, the present invention provides a composition comprising  
30 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:72;

(b) a fragment of the amino acid sequence of SEQ ID NO:72, the fragment comprising eight contiguous amino acids of SEQ ID NO:72; and

(c) the amino acid sequence encoded by the cDNA insert of clone dj167\_2 deposited under accession number ATCC 98818; the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:72. In further preferred  
 5 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:72, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:72 having biological activity, the fragment comprising the amino acid sequence  
 10 from amino acid 195 to amino acid 204 of SEQ ID NO:72.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73;
- 15 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490;
- (d) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343;
- 20 (e) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (f) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- 25 (g) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090;
- (h) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;
- 30 (i) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74;

(j) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:74;

5 (k) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(h) above;

(l) a polynucleotide which encodes a species homologue of the protein of (i) or (j) above ;

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j); and

10 (n) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(j) and that has a length that is at least 25% of the length of SEQ ID NO:73.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73  
15 from nucleotide 1485 to nucleotide 4490; the nucleotide sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343; the nucleotide sequence of the full-length protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090; or the nucleotide sequence of a mature protein coding sequence of clone dj167\_19 deposited under accession number ATCC 207090. In other preferred embodiments, the  
20 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090. In yet other preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a  
25 polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:74, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid  
30 sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:73.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:



(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

5 (aa) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

(ab) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

10 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

15 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:73, but excluding the poly(A) tail at the 3' end of SEQ ID NO:73; and

20 (bb) the nucleotide sequence of the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

25 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:73 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:73, but  
30 excluding the poly(A) tail at the 3' end of SEQ ID NO:73. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490, to a nucleotide

sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1383 to nucleotide 4490. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, and extending contiguously from  
5 a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 1485 to nucleotide 4490. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:73 from  
10 nucleotide 3645 to nucleotide 4343, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:73 from nucleotide 3645 to nucleotide 4343.

In other embodiments, the present invention provides a composition comprising  
15 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:74;
- (b) the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036;
- 20 (c) a fragment of the amino acid sequence of SEQ ID NO:74, the fragment comprising eight contiguous amino acids of SEQ ID NO:74; and
- (d) the amino acid sequence encoded by the cDNA insert of clone dj167\_19 deposited under accession number ATCC 207090;

the protein being substantially free from other mammalian proteins. Preferably such  
25 protein comprises the amino acid sequence of SEQ ID NO:74 or the amino acid sequence of SEQ ID NO:74 from amino acid 637 to amino acid 1036. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
30 of SEQ ID NO:74, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:74 having biological activity, the fragment comprising the amino acid sequence from amino acid 513 to amino acid 522 of SEQ ID NO:74.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441;
- 5 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- 10 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818;
- 15 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:76;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:76;
- 20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- 25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:75.
- 30

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441; the nucleotide sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441; the nucleotide sequence of the full-length protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818; or the

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nucleotide sequence of a mature protein coding sequence of clone dw665\_4 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818. In further preferred  
5 embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having  
10 biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:75.

Further embodiments of the invention provide isolated polynucleotides produced  
15 according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

20 (aa) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(ab) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

25 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
    - (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 30

(ba) SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75; and

(bb) the nucleotide sequence of the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

5 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:75 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:75, but excluding the poly(A) tail at the 3' end of SEQ ID NO:75. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 71 to nucleotide 1441. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:75 from nucleotide 152 to nucleotide 1441.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:76;

(b) a fragment of the amino acid sequence of SEQ ID NO:76, the fragment comprising eight contiguous amino acids of SEQ ID NO:76; and

(c) the amino acid sequence encoded by the cDNA insert of clone dw665\_4 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:76. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment preferably

comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:76, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:76 having biological activity, the fragment comprising the amino acid sequence from amino acid 223 to amino acid 232 of SEQ ID NO:76.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:77;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID  
10 NO:77 from nucleotide 78 to nucleotide 1592;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (d) a polynucleotide encoding the full-length protein encoded by the  
15 cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA  
20 insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:78;
- (h) a polynucleotide encoding a protein comprising a fragment of the  
25 amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:78;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein  
of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any  
30 one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:77.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592; the nucleotide sequence of the full-length protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx146\_12 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:77.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
    - (ab) the nucleotide sequence of the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

- 5 (ba) SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77; and
- (bb) the nucleotide sequence of the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- 10 (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:77 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:77, but excluding the poly(A) tail at the 3' end of SEQ ID NO:77. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:77 from nucleotide 78 to nucleotide 1592.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:78;
- (b) a fragment of the amino acid sequence of SEQ ID NO:78, the fragment comprising eight contiguous amino acids of SEQ ID NO:78; and
- (c) the amino acid sequence encoded by the cDNA insert of clone dx146\_12 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:78. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment preferably



comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:78, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:78 having biological activity, the fragment comprising the amino acid sequence from amino acid 247 to amino acid 256 of SEQ ID NO:78.

5 In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

(a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79;

10 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948;

15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:80;

25 (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:80;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

30 (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:79.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948; the nucleotide sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948; the nucleotide sequence of the full-length protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone dx219\_13 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:80, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:79.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(ab) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79; and

(bb) the nucleotide sequence of the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:79 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:79, but excluding the poly(A) tail at the 3' end of SEQ ID NO:79. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 19 to nucleotide 948. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:79 from nucleotide 337 to nucleotide 948.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:80;

(b) a fragment of the amino acid sequence of SEQ ID NO:80, the fragment comprising eight contiguous amino acids of SEQ ID NO:80; and

(c) the amino acid sequence encoded by the cDNA insert of clone dx219\_13 deposited under accession number ATCC 98818;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:80. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
10 of SEQ ID NO:80, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:80 having biological activity, the fragment comprising the amino acid sequence from amino acid 150 to amino acid 159 of SEQ ID NO:80.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

15 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286;

20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;

25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818;

30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:82;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:82;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:81.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286; the nucleotide sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286; the nucleotide sequence of the full-length protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone fm3\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:82, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:81.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(ab) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81; and

(bb) the nucleotide sequence of the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:81 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:81, but excluding the poly(A) tail at the 3' end of SEQ ID NO:81. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 5 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide

5 to nucleotide 286. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:81 from nucleotide 62 to nucleotide 286.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:82;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:82, the fragment comprising eight contiguous amino acids of SEQ ID NO:82; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone fm3\_1 deposited under accession number ATCC 98818;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:82. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:82, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:82 having biological activity, the fragment comprising the amino acid sequence from amino acid 42 to amino acid 51 of SEQ ID NO:82.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:83 from nucleotide 333 to nucleotide 572;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:84;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:84;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:83.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572; the nucleotide sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572; the nucleotide sequence of the full-length protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone h225\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:84, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the



fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:83.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:83; and

(ab) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

20 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:83; and

25 (bb) the nucleotide sequence of the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:83 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:83. Also preferably the polynucleotide isolated according to the above process comprises a

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nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 141 to nucleotide 572. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:83 from nucleotide 333 to nucleotide 572.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 15 (a) the amino acid sequence of SEQ ID NO:84;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:84, the fragment comprising eight contiguous amino acids of SEQ ID NO:84; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone h225\_1 deposited under accession number ATCC 98818;
- 20 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:84. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 25 of SEQ ID NO:84, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:84 having biological activity, the fragment comprising the amino acid sequence from amino acid 67 to amino acid 76 of SEQ ID NO:84.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 30 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:86;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:86;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:85.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210; the nucleotide sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210; the nucleotide sequence of the full-length protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone kj320\_1 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a polynucleotide encoding  
5 a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:85.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

(ab) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85; and

30 (bb) the nucleotide sequence of the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:85 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:85, but excluding the poly(A) tail at the 3' end of SEQ ID NO:85. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:85 from nucleotide  
10 391 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 391 to nucleotide 3210. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:85 from nucleotide 505 to nucleotide 3210, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:85 from nucleotide 505 to nucleotide 3210.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:86;
- (b) a fragment of the amino acid sequence of SEQ ID NO:86, the fragment comprising eight contiguous amino acids of SEQ ID NO:86; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone kj320\_1 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:86. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:86, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:86 having biological activity, the fragment comprising the amino acid sequence from amino acid 465 to amino acid 474 of SEQ ID NO:86.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:88;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:88;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:87.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899; the nucleotide sequence of SEQ ID NO:87

from nucleotide 522 to nucleotide 899; the nucleotide sequence of the full-length protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone ml236\_5 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:87.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(ab) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87; and

(bb) the nucleotide sequence of the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a  
10 nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:87 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:87, but excluding the poly(A) tail at the 3' end of SEQ ID NO:87. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 42 to nucleotide 899. Also preferably the polynucleotide isolated according to the above  
20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:87 from nucleotide 522 to nucleotide 899.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:88;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:88, the fragment comprising eight contiguous amino acids of SEQ ID NO:88; and

(c) the amino acid sequence encoded by the cDNA insert of clone ml236\_5 deposited under accession number ATCC 98818;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:88. In further preferred



embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:88, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:88 having biological activity, the fragment comprising the amino acid sequence from amino acid 138 to amino acid 147 of SEQ ID NO:88.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:90;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:90;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:89.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452; the nucleotide sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452; the nucleotide sequence of the full-length protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818; or the nucleotide sequence of a mature protein coding sequence of clone pu282\_10 deposited under accession number ATCC 98818. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:89.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

(ab) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:89, but excluding the poly(A) tail at the 3' end of SEQ ID NO:89; and

10 (bb) the nucleotide sequence of the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:89 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:89, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:89. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 6 to nucleotide 452. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:89 from  
30 nucleotide 399 to nucleotide 452, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:89 from nucleotide 399 to nucleotide 452.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:90;
- (b) a fragment of the amino acid sequence of SEQ ID NO:90, the fragment comprising eight contiguous amino acids of SEQ ID NO:90; and
- (c) the amino acid sequence encoded by the cDNA insert of clone pu282\_10 deposited under accession number ATCC 98818;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:90. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment preferably

10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:90, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:90 having biological activity, the fragment comprising the amino acid sequence from amino acid 69 to amino acid 78 of SEQ ID NO:90.

In one embodiment, the present invention provides a composition comprising an

15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:92;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:92;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:91.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179; the nucleotide sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179; the nucleotide sequence of the full-length protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone at94\_2 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:92, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:91.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(ab) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91; and

(bb) the nucleotide sequence of the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:91 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:91, but excluding the poly(A) tail at the 3' end of SEQ ID NO:91. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 4 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide

4 to nucleotide 1179. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:91 from nucleotide 682 to nucleotide 1179.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:92;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:92, the fragment comprising eight contiguous amino acids of SEQ ID NO:92; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone at94\_2 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:92. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:92, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:92 having biological activity, the fragment comprising the amino acid sequence from amino acid 191 to amino acid 200 of SEQ ID NO:92.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:94;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:94;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:93.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077; the nucleotide sequence of the full-length protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bf169\_13 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:94, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.



Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:93.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
  - (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:93, but excluding the poly(A) tail at the
    - 10 3' end of SEQ ID NO:93; and
    - (ab) the nucleotide sequence of the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
    - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
    - 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
  - (i) preparing one or more polynucleotide primers that
  - 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:93, but excluding the poly(A) tail at the
    - 3' end of SEQ ID NO:93; and
    - (bb) the nucleotide sequence of the cDNA insert of clone
    - 25 bf169\_13 deposited under accession number ATCC 98822;
    - (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
    - (iii) amplifying human DNA sequences; and
    - (iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:93 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:93, but excluding the poly(A) tail at the 3' end of SEQ ID NO:93. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:93 from nucleotide 56 to nucleotide 2077.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:94;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:94, the fragment comprising eight contiguous amino acids of SEQ ID NO:94; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bf169\_13 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:94. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:94, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:94 having biological activity, the fragment comprising the amino acid sequence from amino acid 332 to amino acid 341 of SEQ ID NO:94.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;
- 30 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822;

(f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:96;

(h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:96;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

(k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:95.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735; the nucleotide sequence of the full-length protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bl152\_12 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:96, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:95.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:95, but excluding the poly(A) tail at the
- 10 3' end of SEQ ID NO:95; and
- (ab) the nucleotide sequence of the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that
- 20 hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95; and
- (bb) the nucleotide sequence of the cDNA insert of clone
- 25 bl152\_12 deposited under accession number ATCC 98822;
- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:95 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:95, but excluding the poly(A) tail at the 3' end of SEQ ID NO:95. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:95 from nucleotide 124 to nucleotide 735.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:96;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:96, the fragment comprising eight contiguous amino acids of SEQ ID NO:96; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bl152\_12 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:96. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:96, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:96 having biological activity, the fragment comprising the amino acid sequence from amino acid 97 to amino acid 106 of SEQ ID NO:96.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession
- 30 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;

- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822;
  - (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
  - (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:98;
  - (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:98;
  - (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
  - (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
  - (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
  - (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:97.
- Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816; the nucleotide sequence of the full-length protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone bz578\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:98, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:97.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 5 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (ab) the nucleotide sequence of the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- 15 (iii) isolating the DNA polynucleotides detected with the probe(s);

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (ba) SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97; and
- (bb) the nucleotide sequence of the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- 25 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

- 30 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:97 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:97, but excluding the poly(A) tail at the 3' end of SEQ ID NO:97. Also preferably the

polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:97 from nucleotide 526 to nucleotide 816.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- 10 (a) the amino acid sequence of SEQ ID NO:98;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:98, the fragment comprising eight contiguous amino acids of SEQ ID NO:98; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone bz578\_1 deposited under accession number ATCC 98822;
- 15 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:98. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids
- 20 of SEQ ID NO:98, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:98 having biological activity, the fragment comprising the amino acid sequence from amino acid 43 to amino acid 52 of SEQ ID NO:98.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 25 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID
- 30 NO:99 from nucleotide 765 to nucleotide 992;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;



- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:100;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:100;
- (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:99.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992; the nucleotide sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992; the nucleotide sequence of the full-length protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cb123\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:100, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:100

having biological activity, the fragment comprising the amino acid sequence from amino acid 61 to amino acid 70 of SEQ ID NO:100.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:99.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(ab) the nucleotide sequence of the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:99, but excluding the poly(A) tail at the 3' end of SEQ ID NO:99; and

(bb) the nucleotide sequence of the cDNA insert of clone cb123\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:99, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ

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ID NO:99 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:99 , but  
excluding the poly(A) tail at the 3' end of SEQ ID NO:99. Also preferably the  
polynucleotide isolated according to the above process comprises a nucleotide sequence  
corresponding to the cDNA sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide  
5 992, and extending contiguously from a nucleotide sequence corresponding to the 5' end  
of said sequence of SEQ ID NO:99 from nucleotide 597 to nucleotide 992, to a nucleotide  
sequence corresponding to the 3' end of said sequence of SEQ ID NO:99 from nucleotide  
597 to nucleotide 992. Also preferably the polynucleotide isolated according to the above  
process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
10 NO:99 from nucleotide 765 to nucleotide 992, and extending contiguously from a  
nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:99 from  
nucleotide 765 to nucleotide 992, to a nucleotide sequence corresponding to the 3' end of  
said sequence of SEQ ID NO:99 from nucleotide 765 to nucleotide 992.

In other embodiments, the present invention provides a composition comprising  
15 a protein, wherein said protein comprises an amino acid sequence selected from the group  
consisting of:

- (a) the amino acid sequence of SEQ ID NO:100;
- (b) a fragment of the amino acid sequence of SEQ ID NO:100, the  
fragment comprising eight contiguous amino acids of SEQ ID NO:100; and
- 20 (c) the amino acid sequence encoded by the cDNA insert of clone  
cb123\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such  
protein comprises the amino acid sequence of SEQ ID NO:100. In further preferred  
embodiments, the present invention provides a protein comprising a fragment of the  
25 amino acid sequence of SEQ ID NO:100 having biological activity, the fragment preferably  
comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids  
of SEQ ID NO:100, or a protein comprising a fragment of the amino acid sequence of SEQ  
ID NO:100 having biological activity, the fragment comprising the amino acid sequence  
from amino acid 61 to amino acid 70 of SEQ ID NO:100.

30 In one embodiment, the present invention provides a composition comprising an  
isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID  
NO:101;

- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:102;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:102;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:101.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480; the nucleotide sequence of the full-length protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ch245\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein

comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102  
5 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:101.

Further embodiments of the invention provide isolated polynucleotides produced  
10 according to a process selected from the group consisting of:

(a) a process comprising the steps of:  
(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

15 (aa) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

(ab) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101; and

30 (bb) the nucleotide sequence of the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:101 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:101, but excluding the poly(A) tail at the 3' end of SEQ ID NO:101. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:101 from nucleotide 181 to nucleotide 480.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:102;
- (b) a fragment of the amino acid sequence of SEQ ID NO:102, the fragment comprising eight contiguous amino acids of SEQ ID NO:102; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ch245\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:102. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:102, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:102 having biological activity, the fragment comprising the amino acid sequence from amino acid 45 to amino acid 54 of SEQ ID NO:102.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541;

(c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;

5 (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;

(e) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822;

10 (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:104;

15 (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:104;

(i) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(f) above;

(j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;

20 (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:103.

25 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541; the nucleotide sequence of the full-length protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cj378\_3 deposited under accession number ATCC 98822. In other preferred embodiments, the  
30 polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most

preferably thirty) contiguous amino acids of SEQ ID NO:104, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

5 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:103.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- (a) a process comprising the steps of:
  - 10 (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (aa) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - 15 (ab) the nucleotide sequence of the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
  - (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
  - 20 (iii) isolating the DNA polynucleotides detected with the probe(s);
- and
- (b) a process comprising the steps of:
  - 25 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
    - (ba) SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103; and
    - (bb) the nucleotide sequence of the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
  - 30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
  - (iii) amplifying human DNA sequences; and
  - (iv) isolating the polynucleotide products of step (b)(iii).



Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:103 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:103, but excluding the poly(A) tail at the 3' end of SEQ ID NO:103. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:103 from nucleotide 281 to nucleotide 541.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:104;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:104, the fragment comprising eight contiguous amino acids of SEQ ID NO:104; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone cj378\_3 deposited under accession number ATCC 98822;
- the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:104. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:104, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:104 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:104.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349;

(d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:106;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:106;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:105.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202; the nucleotide sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349; the nucleotide sequence of the full-length protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone cw1481\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822. In further preferred

embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a polynucleotide  
5 encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:105.

10 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group  
15 consisting of:

(aa) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(ab) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

20 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

25 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105; and

(bb) the nucleotide sequence of the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

30 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105, and  
5 extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:105 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:105, but excluding the poly(A) tail at the 3' end of SEQ ID NO:105. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:105 from nucleotide  
10 2202, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 586 to nucleotide 2202. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID  
15 NO:105 from nucleotide 401 to nucleotide 2349, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:105 from nucleotide 401 to nucleotide 2349.

In other embodiments, the present invention provides a composition comprising  
20 a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:106;
- (b) a fragment of the amino acid sequence of SEQ ID NO:106, the fragment comprising eight contiguous amino acids of SEQ ID NO:106; and
- 25 (c) the amino acid sequence encoded by the cDNA insert of clone cw1481\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:106. In further preferred embodiments, the present invention provides a protein comprising a fragment of the  
30 amino acid sequence of SEQ ID NO:106 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:106, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:106 having biological activity, the fragment comprising the amino acid sequence from amino acid 264 to amino acid 273 of SEQ ID NO:106.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107;
- 5 (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905;
- 10 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 15 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;
- 20 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:108;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:108;
- 25 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;
- (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and
- 30 (m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:107.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905; the nucleotide sequence of SEQ ID NO:107

from nucleotide 146 to nucleotide 2905; the nucleotide sequence of the full-length protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone dd119\_4 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:107.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(ab) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107; and

(bb) the nucleotide sequence of the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:107 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:107, but excluding the poly(A) tail at the 3' end of SEQ ID NO:107. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence

15 corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 29 to nucleotide 2905. Also preferably the polynucleotide isolated according to the above

20 process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:107 from nucleotide 146 to nucleotide 2905.

25 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:108;

30 (b) a fragment of the amino acid sequence of SEQ ID NO:108, the fragment comprising eight contiguous amino acids of SEQ ID NO:108; and

(c) the amino acid sequence encoded by the cDNA insert of clone dd119\_4 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:108. In further preferred

embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:108, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:108 having biological activity, the fragment comprising the amino acid sequence from amino acid 474 to amino acid 483 of SEQ ID NO:108.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 10 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369;
- 15 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- 20 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;
- 25 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:110;
- (i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:110;
- 30 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;
- (k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;



(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:109.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369; the nucleotide sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369; the nucleotide sequence of the full-length protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone df202\_3 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:109.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

(ab) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

5 (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:109, but excluding the poly(A) tail at the 3' end of SEQ ID NO:109; and

10 (bb) the nucleotide sequence of the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

15 (iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:109 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:109, but  
20 excluding the poly(A) tail at the 3' end of SEQ ID NO:109. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369, to a nucleotide  
25 sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 16 to nucleotide 369. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:109 from  
30 nucleotide 103 to nucleotide 369, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:109 from nucleotide 103 to nucleotide 369.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:110;
- (b) a fragment of the amino acid sequence of SEQ ID NO:110, the fragment comprising eight contiguous amino acids of SEQ ID NO:110; and
- (c) the amino acid sequence encoded by the cDNA insert of clone df202\_3 deposited under accession number ATCC 98822;

5 the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:110. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment preferably  
10 comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:110, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:110 having biological activity, the fragment comprising the amino acid sequence from amino acid 54 to amino acid 63 of SEQ ID NO:110.

In one embodiment, the present invention provides a composition comprising an  
15 isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539;
- 20 (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- 25 (e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822;
- 30 (g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;
- (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:112;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:112;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:111.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539; the nucleotide sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539; the nucleotide sequence of the full-length protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone km225\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:111.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(ab) the nucleotide sequence of the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

(b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(ba) SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111; and

(bb) the nucleotide sequence of the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:111 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:111, but excluding the poly(A) tail at the 3' end of SEQ ID NO:111. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2192 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111

from nucleotide 2192 to nucleotide 2539. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:111 from nucleotide 2255 to nucleotide 2539.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:112;
- (b) a fragment of the amino acid sequence of SEQ ID NO:112, the fragment comprising eight contiguous amino acids of SEQ ID NO:112; and
- (c) the amino acid sequence encoded by the cDNA insert of clone km225\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:112. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:112, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:112 having biological activity, the fragment comprising the amino acid sequence from amino acid 53 to amino acid 62 of SEQ ID NO:112.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030;
- (c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030;
- (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:114;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:114;

(j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

(l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:113.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030; the nucleotide sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030; the nucleotide sequence of the full length protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone mj301\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114

having biological activity, the fragment comprising the amino acid sequence from amino acid 44 to amino acid 53 of SEQ ID NO:114.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:113.

5 Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a) a process comprising the steps of:

(i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

10 (aa) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(ab) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

15 (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii) isolating the DNA polynucleotides detected with the probe(s);

and

20 (b) a process comprising the steps of:

(i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

25 (ba) SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113; and

(bb) the nucleotide sequence of the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

(ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

30 (iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ



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ID NO:113 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:113, but excluding the poly(A) tail at the 3' end of SEQ ID NO:113. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:113 from nucleotide 1734 to  
5 nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 1734 to nucleotide 2030. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the  
10 cDNA sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:113 from nucleotide 1965 to nucleotide 2030.

15 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:114;
- (b) a fragment of the amino acid sequence of SEQ ID NO:114, the  
20 fragment comprising eight contiguous amino acids of SEQ ID NO:114; and
- (c) the amino acid sequence encoded by the cDNA insert of clone mj301\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:114. In further preferred  
25 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:114, or a protein comprising a fragment of the amino acid sequence of SEQ ID NO:114 having biological activity, the fragment comprising the amino acid sequence  
30 from amino acid 44 to amino acid 53 of SEQ ID NO:114.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115;

(b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350;

(c) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350;

5 (d) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;

(e) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

10 (f) a polynucleotide comprising the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822;

(g) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

15 (h) a polynucleotide encoding a protein comprising the amino acid sequence of SEQ ID NO:116;

(i) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:116;

20 (j) a polynucleotide which is an allelic variant of a polynucleotide of (a)-(g) above;

(k) a polynucleotide which encodes a species homologue of the protein of (h) or (i) above ;

25 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i); and

(m) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(i) and that has a length that is at least 25% of the length of SEQ ID NO:115.

30 Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350; the nucleotide sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350; the nucleotide sequence of the full-length protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone ml10\_7 deposited under accession number ATCC 98822. In other preferred embodiments, the

polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822. In further preferred embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

10 Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:115.

Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

- 15 (a) a process comprising the steps of:
- (i) preparing one or more polynucleotide probes that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- (aa) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- 20 (ab) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;
- (ii) hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and
- (iii) isolating the DNA polynucleotides detected with the probe(s);
- 25

and

- (b) a process comprising the steps of:
- (i) preparing one or more polynucleotide primers that hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:
- 30 (ba) SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115; and
- (bb) the nucleotide sequence of the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

- (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;
- (iii) amplifying human DNA sequences; and
- (iv) isolating the polynucleotide products of step (b)(iii).

5 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:115 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:115, but excluding the poly(A) tail at the 3' end of SEQ ID NO:115. Also preferably the  
10 polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 799 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:115 from nucleotide  
15 799 to nucleotide 1350. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350, to a nucleotide sequence corresponding to the 3' end  
20 of said sequence of SEQ ID NO:115 from nucleotide 925 to nucleotide 1350.

In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:116;
- 25 (b) a fragment of the amino acid sequence of SEQ ID NO:116, the fragment comprising eight contiguous amino acids of SEQ ID NO:116; and
- (c) the amino acid sequence encoded by the cDNA insert of clone ml10\_7 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such  
30 protein comprises the amino acid sequence of SEQ ID NO:116. In further preferred embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:116 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:116, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:116 having biological activity, the fragment comprising the amino acid sequence from amino acid 87 to amino acid 96 of SEQ ID NO:116.

In one embodiment, the present invention provides a composition comprising an isolated polynucleotide selected from the group consisting of:

- 5 (a) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117;
- (b) a polynucleotide comprising the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094;
- (c) a polynucleotide comprising the nucleotide sequence of the full-length protein coding sequence of clone my340\_1 deposited under accession  
10 number ATCC 98822;
- (d) a polynucleotide encoding the full-length protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (e) a polynucleotide comprising the nucleotide sequence of a mature  
15 protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822;
- (f) a polynucleotide encoding a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;
- (g) a polynucleotide encoding a protein comprising the amino acid  
20 sequence of SEQ ID NO:118;
- (h) a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising eight contiguous amino acids of SEQ ID NO:118;
- (i) a polynucleotide which is an allelic variant of a polynucleotide of  
25 (a)-(f) above;
- (j) a polynucleotide which encodes a species homologue of the protein of (g) or (h) above ;
- (k) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h); and
- 30 (l) a polynucleotide that hybridizes under stringent conditions to any one of the polynucleotides specified in (a)-(h) and that has a length that is at least 25% of the length of SEQ ID NO:117.

Preferably, such polynucleotide comprises the nucleotide sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094; the nucleotide sequence of the full-length

protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822; or the nucleotide sequence of a mature protein coding sequence of clone my340\_1 deposited under accession number ATCC 98822. In other preferred embodiments, the polynucleotide encodes the full-length or a mature protein encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822. In further preferred  
5       embodiments, the present invention provides a polynucleotide encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a polynucleotide  
10       encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

Other embodiments provide the gene corresponding to the cDNA sequence of SEQ ID NO:117.

15       Further embodiments of the invention provide isolated polynucleotides produced according to a process selected from the group consisting of:

(a)     a process comprising the steps of:

(i)     preparing one or more polynucleotide probes that hybridize  
20       in 6X SSC at 65 degrees C to a nucleotide sequence selected from the group consisting of:

(aa)    SEQ ID NO:117, but excluding the poly(A) tail at the  
3' end of SEQ ID NO:117; and

(ab)    the nucleotide sequence of the cDNA insert of clone  
my340\_1 deposited under accession number ATCC 98822;

25       (ii)    hybridizing said probe(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C; and

(iii)   isolating the DNA polynucleotides detected with the  
probe(s);

and

30       (b)     a process comprising the steps of:

(i)     preparing one or more polynucleotide primers that  
hybridize in 6X SSC at 65 degrees C to a nucleotide sequence selected from  
the group consisting of:

(ba) SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117; and

(bb) the nucleotide sequence of the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;

5 (ii) hybridizing said primer(s) to human genomic DNA in conditions at least as stringent as 4X SSC at 50 degrees C;

(iii) amplifying human DNA sequences; and

(iv) isolating the polynucleotide products of step (b)(iii).

10 Preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence corresponding to the cDNA sequence of SEQ ID NO:117, and extending contiguously from a nucleotide sequence corresponding to the 5' end of SEQ ID NO:117 to a nucleotide sequence corresponding to the 3' end of SEQ ID NO:117, but excluding the poly(A) tail at the 3' end of SEQ ID NO:117. Also preferably the polynucleotide isolated according to the above process comprises a nucleotide sequence  
15 corresponding to the cDNA sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, and extending contiguously from a nucleotide sequence corresponding to the 5' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094, to a nucleotide sequence corresponding to the 3' end of said sequence of SEQ ID NO:117 from nucleotide 837 to nucleotide 1094.

20 In other embodiments, the present invention provides a composition comprising a protein, wherein said protein comprises an amino acid sequence selected from the group consisting of:

(a) the amino acid sequence of SEQ ID NO:118;

(b) a fragment of the amino acid sequence of SEQ ID NO:118, the  
25 fragment comprising eight contiguous amino acids of SEQ ID NO:118; and

(c) the amino acid sequence encoded by the cDNA insert of clone my340\_1 deposited under accession number ATCC 98822;

the protein being substantially free from other mammalian proteins. Preferably such protein comprises the amino acid sequence of SEQ ID NO:118. In further preferred  
30 embodiments, the present invention provides a protein comprising a fragment of the amino acid sequence of SEQ ID NO:118 having biological activity, the fragment preferably comprising eight (more preferably twenty, most preferably thirty) contiguous amino acids of SEQ ID NO:118, or a protein comprising a fragment of the amino acid sequence of SEQ

ID NO:118 having biological activity, the fragment comprising the amino acid sequence from amino acid 38 to amino acid 47 of SEQ ID NO:118.

In certain preferred embodiments, the polynucleotide is operably linked to an expression control sequence. The invention also provides a host cell, including bacterial, yeast, insect and mammalian cells, transformed with such polynucleotide compositions. Also provided by the present invention are organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein.

Processes are also provided for producing a protein, which comprise:

- (a) growing a culture of the host cell transformed with such polynucleotide compositions in a suitable culture medium; and
- (b) purifying the protein from the culture.

The protein produced according to such methods is also provided by the present invention.

Protein compositions of the present invention may further comprise a pharmaceutically acceptable carrier. Compositions comprising an antibody which specifically reacts with such protein are also provided by the present invention.

Methods are also provided for preventing, treating or ameliorating a medical condition which comprises administering to a mammalian subject a therapeutically effective amount of a composition comprising a protein of the present invention and a pharmaceutically acceptable carrier.

#### BRIEF DESCRIPTION OF THE DRAWINGS

Figures 1A and 1B are schematic representations of the pED6 and pNOTs vectors, respectively, used for deposit of clones disclosed herein.

#### DETAILED DESCRIPTION

##### ISOLATED PROTEINS AND POLYNUCLEOTIDES

Nucleotide and amino acid sequences, as presently determined, are reported below for each clone and protein disclosed in the present application. The nucleotide sequence of each clone can readily be determined by sequencing of the deposited clone in accordance with known methods. The predicted amino acid sequence (both full-length and mature forms) can then be determined from such nucleotide sequence. The amino acid sequence of the protein encoded by a particular clone can also be determined by



expression of the clone in a suitable host cell, collecting the protein and determining its sequence. For each disclosed protein applicants have identified what they have determined to be the reading frame best identifiable with sequence information available at the time of filing.

5 As used herein a "secreted" protein is one which, when expressed in a suitable host cell, is transported across or through a membrane, including transport as a result of signal sequences in its amino acid sequence. "Secreted" proteins include without limitation proteins secreted wholly (e.g., soluble proteins) or partially (e.g., receptors) from the cell in which they are expressed. "Secreted" proteins also include without limitation proteins  
10 which are transported across the membrane of the endoplasmic reticulum.

#### Clone "bn365\_53"

A polynucleotide of the present invention has been identified as clone "bn365\_53". bn365\_53 was isolated from a human adult placenta cDNA library using methods which  
15 are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bn365\_53 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bn365\_53 protein").

20 The nucleotide sequence of bn365\_53 as presently determined is reported in SEQ ID NO:1, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bn365\_53 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:2.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 bn365\_53 should be approximately 650 bp.

The nucleotide sequence disclosed herein for bn365\_53 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bn365\_53 demonstrated at least some similarity with sequences identified as AA242967 (zr65g11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone  
30 668324 5') and N40141 (yw73c12.r1 Homo sapiens cDNA clone 257878 5'). The predicted amino acid sequence disclosed herein for bn365\_53 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bn365\_53 protein demonstrated at least some similarity to sequences identified as D63484 (KIAA0150 protein [Homo sapiens]) and to the GAGE-1 to GAGE-6 family of

human proteins expressed in tumors (GenBank Accession Numbers U19142-U19147). The amino acid sequence of SEQ ID NO:2 contains two RGD (Arg-Gly-Asp) motifs (around residues 12 and 75): the sequence Arg-Gly-Asp, found in fibronectin, is crucial for its interaction with its cell surface receptor, an integrin. What has been called the 'RGD' tripeptide is also found in the sequences of a number of other proteins, where it has been shown to play a role in cell adhesion. These proteins are: some forms of collagens, fibrinogen, vitronectin, von Willebrand factor (VWF), snake disintegrins, and slime mold discoidins. Based upon sequence similarity, bn365\_53 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bn365\_53 indicates that it may contain one or more repetitive elements.

#### Clone "bo342\_2"

A polynucleotide of the present invention has been identified as clone "bo342\_2". bo342\_2 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bo342\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bo342\_2 protein").

The nucleotide sequence of bo342\_2 as presently determined is reported in SEQ ID NO:3, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bo342\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:4. Amino acids 372 to 384 of SEQ ID NO:4 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 385. Amino acids 1 to 13 are also a possible leader/signal sequence, with the predicted mature amino acid sequence beginning in that case at amino acid 14. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the bo342\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bo342\_2 should be approximately 2600 bp.

The nucleotide sequence disclosed herein for bo342\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bo342\_2 demonstrated at least some similarity with sequences

identified as AA306000 (EST177027 Jurkat T-cells VI Homo sapiens cDNA 5' end) and W94256 (ze12b02.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 358731 3' similar to contains Alu repetitive element). Based upon sequence similarity, bo342\_2 proteins and each similar protein or peptide may share at least some activity. The  
5 TopPredII computer program predicts six potential transmembrane domains within the bo342\_2 protein sequence, centered around amino acids 300, 320, 380, 410, 430, and 490 of SEQ ID NO:4, respectively. The nucleotide sequence of bo342\_2 indicates that it may contain Alu or other repetitive elements.

10 Clone "dn721\_8"

A polynucleotide of the present invention has been identified as clone "dn721\_8". dn721\_8 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
15 analysis of the amino acid sequence of the encoded protein. dn721\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn721\_8 protein").

The nucleotide sequence of dn721\_8 as presently determined is reported in SEQ ID NO:5, and includes a poly(A) tail. What applicants presently believe to be the proper  
20 reading frame and the predicted amino acid sequence of the dn721\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:6.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn721\_8 should be approximately 2900 bp.

The nucleotide sequence disclosed herein for dn721\_8 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn721\_8 demonstrated at least some similarity with sequences identified as H63637 (yr34b12.r1 Homo sapiens cDNA clone 207167 5'), N31598 (yy20b12.s1 Homo sapiens cDNA clone 271775 3'), and R61419 (yh15e05.r1 Homo sapiens cDNA clone 37671 5'). Based upon sequence similarity, dn721\_8 proteins and each similar  
30 protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the dn721\_8 protein sequence, one centered around amino acid 269 and another around amino acid 457 of SEQ ID NO:6.

Clone "dn834\_1"

A polynucleotide of the present invention has been identified as clone "dn834\_1". dn834\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dn834\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dn834\_1 protein").

The nucleotide sequence of dn834\_1 as presently determined is reported in SEQ  
10 ID NO:7, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dn834\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:8.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dn834\_1 should be approximately 900 bp.

15 The nucleotide sequence disclosed herein for dn834\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dn834\_1 demonstrated at least some similarity with sequences identified as AA544005 (vj83h07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone 935677 5'), AL022163 (Human DNA sequence \*\*\* SEQUENCING  
20 IN PROGRESS \*\*\* from clone 551E13; HTGS phase 1), L44560 (Homo sapiens thymus mRNA (randomly primed, normalized), single-pass sequence), and T72271 (Human B cell surface antigen cDNA). The predicted amino acid sequence disclosed herein for dn834\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dn834\_1 protein demonstrated at least some  
25 similarity to sequences identified as R47496 (Translated sequence of domains I and II of celD cDNA in clone pCNP4). Based upon sequence similarity, dn834\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dn834\_1 protein sequence, centered around amino acids 59, 84, and 145 of SEQ ID NO:8, respectively.

30 dn834\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 18 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "pd278\_5"

A polynucleotide of the present invention has been identified as clone "pd278\_5". A cDNA clone was first isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or  
5 was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate pd278\_5 from a human adult kidney cDNA library. pd278\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pd278\_5 protein").

10 The nucleotide sequence of pd278\_5 as presently determined is reported in SEQ ID NO:9, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pd278\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:10. Amino acids 61 to 73 of SEQ ID NO:10 are a predicted leader/signal sequence, with the predicted  
15 mature amino acid sequence beginning at amino acid 74. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pd278\_5 protein.

There are two additional and mutually overlapping possible open reading frames  
20 close to the 5' end of SEQ ID NO:9 (bases 82 - 420 and bases 119 - 414). The translated open reading frame of bases 119 - 414 has a predicted leader/signal sequence from amino acid 49 to amino acid 61, with the predicted mature amino acid sequence beginning at amino acid 62. Each of the additional possible open reading frames has a predicted transmembrane domain.

25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pd278\_5 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for pd278\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pd278\_5 demonstrated at least some similarity with sequences  
30 identified as AA292241 (zt50d11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 725781 5'), AA428245 zw51d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773587 3'), AA599487 (ag23f05.s1 Jia bone marrow stroma Homo sapiens cDNA clone 1071201 3'), AA827135 (ob53b03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE 1335053 3'), H54322 (yq90d03.s1 Homo sapiens cDNA clone 203045 3'), and

669050-1190E50  
T22170 (Human gene signature HUMGS03741). The predicted amino acid sequence disclosed herein for pd278\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pd278\_5 protein demonstrated at least some similarity to sequences identified as R13144 (Deleted in  
5 Colorectal Carcinomas) and X13885 (extensin (AA 1-620) [Nicotiana tabacum]). Based upon sequence similarity, pd278\_5 proteins and each similar protein or peptide may share at least some activity.

Clone "pe80\_1"

10 A polynucleotide of the present invention has been identified as clone "pe80\_1". pe80\_1 was isolated from a human adult blood (chronic myelogenous leukemia K562) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded  
15 protein. pe80\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pe80\_1 protein").

The nucleotide sequence of pe80\_1 as presently determined is reported in SEQ ID NO:11, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pe80\_1 protein corresponding  
20 to the foregoing nucleotide sequence is reported in SEQ ID NO:12.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pe80\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pe80\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. pe80\_1 demonstrated at least some similarity with sequences identified as AA291078 (zs47b04.r1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:700591 5'), AA429912 (zw66e06.s1 Soares testis NHT Homo sapiens cDNA clone 781186 3'), H82367 (yv79d06.r1 Homo sapiens cDNA clone 248939 5' similar to contains Alu repetitive element; contains OFR repetitive element), Q60627 (Human brain Expressed  
30 Sequence Tag EST02640), and R20261 (yg20a02.r1 Homo sapiens cDNA clone 32587 5'). Based upon sequence similarity, pe80\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two possible transmembrane domains within the pe80\_1 protein sequence, one centered around amino

acid 58 and another around amino acid 109 of SEQ ID NO:12. The nucleotide sequence of pe80\_1 indicates that it may contain an Alu repetitive element.

Clone "pm113\_1"

5 A polynucleotide of the present invention has been identified as clone "pm113\_1". pm113\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm113\_1 is a  
10 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm113\_1 protein").

The nucleotide sequence of pm113\_1 as presently determined is reported in SEQ ID NO:13, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm113\_1 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:14. Amino acids 41 to 53 of SEQ ID NO:14 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 54. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the  
20 pm113\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm113\_1 should be approximately 1700 bp.

The nucleotide sequence disclosed herein for pm113\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. pm113\_1 demonstrated at least some similarity with sequences identified as AA009482 (zi04c03.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429796 5'), AA350890 (EST58401 Infant brain Homo sapiens cDNA 3' end), AC003030 (Human DNA from chromosome 19-specific cosmid R29828, genomic sequence, complete sequence), H98961 (yx11b02.s1 Homo sapiens cDNA clone 261387 3'), R07796  
30 (yf15e05.r1 Homo sapiens cDNA clone), T22151 (Human gene signature HUMGS03721), and W68491 (zd34h02.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342579 5'). Based upon sequence similarity, pm113\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "pm749\_8"

A polynucleotide of the present invention has been identified as clone "pm749\_8". pm749\_8 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm749\_8 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm749\_8 protein").

The nucleotide sequence of pm749\_8 as presently determined is reported in SEQ ID NO:15, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm749\_8 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:16.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm749\_8 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for pm749\_8 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm749\_8 demonstrated at least some similarity with sequences identified as AA314025 (EST185879 Colon carcinoma (HCC) cell line II Homo sapiens cDNA 5' end) and AA374458 (EST86612 HSC172 cells I Homo sapiens cDNA 5' end). The predicted amino acid sequence disclosed herein for pm749\_8 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm749\_8 protein demonstrated at least some similarity to sequences identified as D89169 (similar to Saccharomyces cerevisiae SCD6 protein, SWISS-PROT Accession Number P45978 [Schizosaccharomyces pombe]) and U30384 (Scd6p [Saccharomyces cerevisiae]). Based upon sequence similarity, pm749\_8 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm749\_8 protein sequence centered around amino acid 138 of SEQ ID NO:16.

Clone "pt31\_4"

A polynucleotide of the present invention has been identified as clone "pt31\_4". pt31\_4 was isolated from a human adult blood (lymphoblastic leukemia MOLT-4) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on



the basis of computer analysis of the amino acid sequence of the encoded protein. pt31\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pt31\_4 protein").

5 The nucleotide sequence of pt31\_4 as presently determined is reported in SEQ ID NO:17, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pt31\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:18. Amino acids 19 to 31 of SEQ ID NO:18 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 32. Due to the hydrophobic nature of the  
10 predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pt31\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pt31\_4 should be approximately 3200 bp.

15 The nucleotide sequence disclosed herein for pt31\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pt31\_4 demonstrated at least some similarity with sequences identified as AA348130 (EST54532 Fetal heart II Homo sapiens cDNA 5' end), AA350691 (EST58082 Infant brain Homo sapiens cDNA 5' end), AC001226 (Genomic sequence from  
20 Human 13, complete sequence), H22773 (ym54c06.r1 Homo sapiens cDNA clone 52351 5'), and R21869 (yh22b10.s1 Homo sapiens cDNA clone 130459 3'). The predicted amino acid sequence disclosed herein for pt31\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pt31\_4 protein demonstrated at least some similarity to sequences identified as U53147 (C01B7.6  
25 [Caenorhabditis elegans]). Based upon sequence similarity, pt31\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five potential transmembrane domains within the pt31\_4 protein sequence, centered around amino acids 90, 110, 210, 410, and 590 of SEQ ID NO:18, respectively.

30

#### Clone "pv296\_5"

A polynucleotide of the present invention has been identified as clone "pv296\_5". pv296\_5 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or

was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pv296\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pv296\_5 protein").

5       The nucleotide sequence of pv296\_5 as presently determined is reported in SEQ ID NO:19, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pv296\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:20.

10       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pv296\_5 should be approximately 1800 bp.

15       The nucleotide sequence disclosed herein for pv296\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pv296\_5 demonstrated at least some similarity with sequences identified as AA022471 (ze70c01.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 364320 3'), AA335246 (EST39647 Epididymus Homo sapiens cDNA 5' end), and AA481308 (zv06a05.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 752816 5'). Based upon sequence similarity, pv296\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pv296\_5 protein sequence centered around amino acid  
20   32 of SEQ ID NO:20.

#### Clone "er311\_20"

25       A polynucleotide of the present invention has been identified as clone "er311\_20". er311\_20 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. er311\_20 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "er311\_20 protein").

30       The nucleotide sequence of er311\_20 as presently determined is reported in SEQ ID NO:21, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the er311\_20 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:22. Amino acids 654 to 666 of SEQ ID NO:22 are a possible leader/signal sequence, with the

predicted mature amino acid sequence beginning at amino acid 667. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the er311\_20 protein.

5 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone er311\_20 should be approximately 2800 bp.

The nucleotide sequence disclosed herein for er311\_20 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. er311\_20 demonstrated at least some similarity with sequences  
10 identified as AF035526 (Mus musculus kanadaplin mRNA, complete cds), R18277 (yg01c06.r1 Homo sapiens cDNA clone 31018 5' similar to SP:ZK632.2 CE00419 COILED COIL PROTEIN), R47371 (Hf060-r Homo sapiens cDNA clone f060-r), and Z40133 (H. sapiens partial cDNA sequence; clone c-1sh08). The predicted amino acid sequence disclosed herein for er311\_20 was searched against the GenPept and GeneSeq  
15 amino acid sequence databases using the BLASTX search protocol. The predicted er311\_20 protein demonstrated at least some similarity to sequences identified as AF035526 (kanadaplin [Mus musculus]) and Z22181 (ZK632.2 [Caenorhabditis elegans]). The mouse kanadaplin protein and the predicted er311\_20 protein both contain polyglutamic acid stretches within their C-terminal portions. Based upon sequence similarity,  
20 er311\_20 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the er311\_20 protein sequence, one centered around amino acid 667 and another at the extreme C-terminus of SEQ ID NO:22.

er311\_20 protein was expressed in a COS cell expression system, and an expressed  
25 protein band of approximately 91 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "fh149\_12"

A polynucleotide of the present invention has been identified as clone "fh149\_12".  
30 fh149\_12 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fh149\_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "fh149\_12 protein").

The nucleotide sequence of fh149\_12 as presently determined is reported in SEQ ID NO:23, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the fh149\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:24. Amino acids 133 to 145 of SEQ ID NO:24 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fh149\_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone fh149\_12 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for fh149\_12 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fh149\_12 demonstrated at least some similarity with sequences identified as AA653557 (ag67b07.s1 Gessler Wilms tumor Homo sapiens cDNA clone 1127989 3'), AA191185 (zq45b09.r1 Stratagene hNT neuron (#937233) Homo sapiens cDNA clone 632633 5'), H20588 (yn63d06.r1 Homo sapiens cDNA clone 173099 5'),  
20 R16294 (yf93b09.r1 Homo sapiens cDNA clone 30087 5'), T08702 (Rat OCT-1 gene), T25120 (Human gene signature HUMGS07278), U38652 (Mus musculus transmembrane transporter (Lx1) mRNA, complete cds), U77086 (Human organic cation transporter 1 (hOCT1) mRNA, complete cds), and Z66539 (H.sapiens creatine transporter gene). The predicted amino acid sequence disclosed herein for fh149\_12 was searched against the  
25 GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted fh149\_12 protein demonstrated at least some similarity to sequences identified as D17546 (Collagen [Mus musculus]), R77676 (Rat OCT-1 protein), and U77086 (organic cation transporter 1 [Homo sapiens]). The fh149\_12 protein also shows some homology to organic cation transporters from rat (GenBank L27651) and pig  
30 (GenBank Y09400) cells. Based upon sequence similarity, fh149\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts eleven potential transmembrane domains within the fh149\_12 protein

sequence, centered around amino acids 40, 112, 139, 162, 200, 229, 349, 376, 405, 436, and 467 of SEQ ID NO:24, respectively.

Clone "pc201\_6"

5 A polynucleotide of the present invention has been identified as clone "pc201\_6". pc201\_6 was isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pc201\_6  
10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pc201\_6 protein").

The nucleotide sequence of pc201\_6 as presently determined is reported in SEQ ID NO:25, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pc201\_6 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:26. Amino acids 20 to 32 of SEQ ID NO:26 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 33. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the  
20 pc201\_6 protein.

A partial cDNA clone related to pc201\_6, pc201\_SP, was also isolated from a human adult retina (retinoblastoma WERI-Rb1) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
25 analysis of the amino acid sequence of the encoded protein. The pc201\_SP clone appears to encode a splice variant of the pc201\_6 protein. The amino acid sequence of the predicted pc201\_SP splice variant protein comprises the amino acid sequence reported in SEQ ID NO:177.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 pc201\_6 should be approximately 2500 bp.

The nucleotide sequence disclosed herein for pc201\_6 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pc201\_6 demonstrated at least some similarity with sequences identified as AA256414 (zr80d11.r1 Soares NhHMPu S1 Homo sapiens cDNA clone

682005 5' similar to WP EEED8.9 CE01893), AA342139 (EST47690 Fetal spleen Homo sapiens cDNA 3' end), AC004085 (Homo sapiens; HTGS phase 1, 72 unordered pieces), AF035950 (Homo sapiens putative DDB p127-associated protein mRNA, partial cds), and H10436 (ym08d09.s1 Homo sapiens cDNA clone 47394 3'). The predicted amino acid  
5 sequence disclosed herein for pc201\_6 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pc201\_6 protein demonstrated at least some similarity to sequences identified as AF035950 (putative DDB p127-associated protein [Homo sapiens]) and U23484 (EEED8.5 [Caenorhabditis elegans]). Based upon sequence similarity, pc201\_6 proteins and each  
10 similar protein or peptide may share at least some activity.

#### Clone "pl87\_1"

A polynucleotide of the present invention has been identified as clone "pl87\_1". pl87\_1 was isolated from a human fetal kidney (293 cell line) cDNA library using methods  
15 which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pl87\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pl87\_1 protein").

20 The nucleotide sequence of pl87\_1 as presently determined is reported in SEQ ID NO:27, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pl87\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:28.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 pl87\_1 should be approximately 700 bp.

The nucleotide sequence disclosed herein for pl87\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pl87\_1 demonstrated at least some similarity with sequences identified as AA371861 (EST83927 Parathyroid gland tumor I Homo sapiens cDNA 5' end)  
30 and AA861863 (ak39e11.s1 Soares testis NHT Homo sapiens cDNA clone IMAGE:1408364 3'). Based upon sequence similarity, pl87\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential

transmembrane domains within the pl87\_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

pl87\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 22 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pm514\_4"

A polynucleotide of the present invention has been identified as clone "pm514\_4". pm514\_4 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm514\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm514\_4 protein").

The nucleotide sequence of pm514\_4 as presently determined is reported in SEQ ID NO:29, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm514\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:30.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm514\_4 should be approximately 3000 bp.

The nucleotide sequence disclosed herein for pm514\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm514\_4 demonstrated at least some similarity with sequences identified as AA393855 (zv64g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 758468 5' similar to WP ZK1248.14 CE02898), AA427943 (zw53d10.s1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 3'), AA434561 (zw53d10.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 773779 5'), W49736 (zc41a03.r1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324844 5'), and U95822 (Human putative transmembrane GTPase mRNA, partial cds). The predicted amino acid sequence disclosed herein for pm514\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted pm514\_4 protein demonstrated at least some similarity to sequences identified as U95822 (putative transmembrane GTPase [Homo sapiens]). Based upon sequence

similarity, pm514\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pm514\_4 protein sequence, centered around amino acid 600 of SEQ ID NO:30.

5           Clone "co155\_12"

A polynucleotide of the present invention has been identified as clone "co155\_12". co155\_12 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10 analysis of the amino acid sequence of the encoded protein. co155\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "co155\_12 protein").

The nucleotide sequence of co155\_12 as presently determined is reported in SEQ ID NO:31, and includes a poly(A) tail. What applicants presently believe to be the proper  
15 reading frame and the predicted amino acid sequence of the co155\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:32. Amino acids 21 to 33 of SEQ ID NO:32 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 34. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
20 should the predicted leader/signal sequence not be separated from the remainder of the co155\_12 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone co155\_12 should be approximately 2700 bp.

The nucleotide sequence disclosed herein for co155\_12 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. co155\_12 demonstrated at least some similarity with sequences identified as AA578373 (nl23d11.s1 NCI\_CGAP\_HSC1 Homo sapiens cDNA clone IMAGE:1041525, mRNA sequence), N43800 (yy42h09.r1 Homo sapiens cDNA clone 273953 5'), and W40418 (zc82c10.r1 Pancreatic Islet Homo sapiens cDNA clone 328818  
30 5', mRNA sequence). The predicted amino acid sequence disclosed herein for co155\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted co155\_12 protein demonstrated at least some similarity to the sequences identified as L12721 (transmembrane domain encoded by



1099-1167) and AF004849 (human serine/threonin protein kinase). Based upon sequence similarity, co155\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential trans-membrane domains within the co155\_12 protein sequence, centered around amino acids  
5 90, 180, 470, 580, and 610 of SEQ ID NO:32, respectively.

#### Clone "fn189\_13"

A polynucleotide of the present invention has been identified as clone "fn189\_13". fn189\_13 was isolated from a human fetal brain cDNA library using methods which are  
10 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fn189\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fn189\_13 protein").

15 The nucleotide sequence of fn189\_13 as presently determined is reported in SEQ ID NO:33, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fn189\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:34. Amino acids 9 to 21 of SEQ ID NO:34 are a predicted leader/signal sequence, with the predicted  
20 mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fn189\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
25 fn189\_13 should be approximately 3800 bp.

The nucleotide sequence disclosed herein for fn189\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fn189\_13 demonstrated at least some similarity with sequences identified as AA144270 (mr14d12.r1 Soares mouse 3NbMS Mus musculus cDNA clone  
30 597431 5') and N27605 (yx44e10.r1 Homo sapiens cDNA clone 264618 5'). The predicted amino acid sequence disclosed herein for fn189\_13 was searched against the GenPept, GeneSeq, and SWISS\_PROT amino acid sequence databases using the BLASTX search protocol. The predicted fn189\_13 protein demonstrated at least some similarity to

sequences identified as P32857 (PROTEIN PTM1 PRECURSOR [Saccharomyces cerevisiae]) and U64598 (weakly similar to S. cerevisiae PTM1 precursor (SP:P32857) [Caenorhabditis elegans]). Based upon sequence similarity, fn189\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts five additional potential transmembrane domains within the fn189\_13 protein sequence, centered around amino acids 225, 260, 340, 360, and 420 of SEQ ID NO:34, respectively.

#### Clone "lv2\_47"

A polynucleotide of the present invention has been identified as clone "lv2\_47". lv2\_47 was isolated from a human adult thyroid cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. lv2\_47 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "lv2\_47 protein").

The nucleotide sequence of lv2\_47 as presently determined is reported in SEQ ID NO:35, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the lv2\_47 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:36. The TopPredII computer program predicts a potential transmembrane domain within the lv2\_47 protein sequence of SEQ ID NO:36, centered around amino acid 60.

Another potential lv2\_47 reading frame and predicted amino acid sequence is encoded by basepairs 365 to 880 of SEQ ID NO:35 and is reported in SEQ ID NO:178. Amino acids 49 to 61 of SEQ ID NO:178 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 62. Due to the hydrophobic nature of this predicted leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the protein of SEQ ID NO:178. The TopPredII computer program predicts two additional potential transmembrane domains within the SEQ ID NO:178 amino acid sequence.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone lv2\_47 should be approximately 1950 bp.

The nucleotide sequence disclosed herein for lv2\_47 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. lv2\_47 demonstrated at least some similarity with sequences identified as AA007293 (zh97f07.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 429253 5'), AA447347 (zw93g06.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784570 5' similar to WP:F43E2.7 CE07243), AA522451 (ng30h09.s1  
5 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:936353), AA526614 (ni52g12.s1 NCI\_CGAP\_Ov2 Homo sapiens cDNA clone 980518), F18178 (H.sapiens EST sequence (002-T4-28) from skeletal muscle, mRNA sequence), H46569 (yo20f10.s1 Homo sapiens cDNA clone 178507 3'), and T22574 (Human gene signature HUMGS04190). Based upon sequence similarity, lv2\_47 proteins and each similar protein or peptide may share  
10 at least some activity.

#### Clone "ml243\_1"

A polynucleotide of the present invention has been identified as clone "ml243\_1". ml243\_1 was isolated from a human adult brain (caudate nucleus) cDNA library using  
15 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml243\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml243\_1 protein").

20 The nucleotide sequence of ml243\_1 as presently determined is reported in SEQ ID NO:37, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml243\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:38. Amino acids 25 to 37 of SEQ ID NO:38 are a predicted leader/signal sequence, with the predicted  
25 mature amino acid sequence beginning at amino acid 38. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml243\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
30 ml243\_1 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml243\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml243\_1 demonstrated at least some similarity with sequences

identified as N66656 (yy71a06.s1 Homo sapiens cDNA clone 278962 3'), R17513 (yg02g12.r1 Homo sapiens cDNA clone 31064 5'), Z83837 (Human DNA sequence from Fosmid 113D11 on chromosome 22q11.2-qter contains ESTs, CpG island), and Z84468 (Human DNA sequence from clone 299D3; HTGS phase 1). Based upon sequence  
5 similarity, ml243\_1 proteins and each similar protein or peptide may share at least some activity.

ml243\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

10

#### Clone "pm96\_9"

A polynucleotide of the present invention has been identified as clone "pm96\_9". pm96\_9 was isolated from a human fetal kidney (293 cell line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.  
15 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pm96\_9 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pm96\_9 protein").

The nucleotide sequence of pm96\_9 as presently determined is reported in SEQ  
20 ID NO:39, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pm96\_9 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:40.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pm96\_9 should be approximately 3600 bp.

25 The nucleotide sequence disclosed herein for pm96\_9 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pm96\_9 demonstrated at least some similarity with sequences identified as AA444024 (zv44d12.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 756503 5'), AA488901 (aa55h09.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone  
30 IMAGE:824897 3'), R16408 (yf40b02.r1 Homo sapiens cDNA clone 129291 5'), T19732 (Human gene signature HUMGS00806), U52112 (Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransfer-

ase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene), and Z82250 (Human DNA sequence from cosmid N86D4 on chromosome 22q12-qter contains STS). Based upon sequence similarity, pm96\_9 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the extreme C-terminus of the pm96\_9 protein sequence (SEQ ID NO:40).

Clone "pu261\_1"

A polynucleotide of the present invention has been identified as clone "pu261\_1". pu261\_1 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pu261\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu261\_1 protein").

The nucleotide sequence of pu261\_1 as presently determined is reported in SEQ ID NO:41, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu261\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:42. Amino acids 116 to 128 of SEQ ID NO:42 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 129. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the pu261\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu261\_1 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pu261\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu261\_1 demonstrated at least some similarity with sequences identified as H16093 (ym20g10.r1 Homo sapiens cDNA clone 48582 5'). Based upon sequence similarity, pu261\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential

transmembrane domain within the pu261\_1 protein sequence centered around amino acid 70 of SEQ ID NO:42.

Clone "pw214\_15"

5 A polynucleotide of the present invention has been identified as clone "pw214\_15". pw214\_15 was isolated from a human adult brain (cerebellum) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. pw214\_15 is a  
10 full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pw214\_15 protein").

The nucleotide sequence of pw214\_15 as presently determined is reported in SEQ ID NO:43, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pw214\_15 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:44.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pw214\_15 should be approximately 1800 bp.

The nucleotide sequence disclosed herein for pw214\_15 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. pw214\_15 demonstrated at least some similarity with sequences identified as AA173391 (zp03a07.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 595284 5'), AA253067 (zr52a10.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 667002 5'), AA523652 ni64d09.s1 NCI\_CGAP\_Pr12 Homo sapiens cDNA clone 981617), and H41832 (yo07b08.r1 Homo sapiens cDNA clone 177207 5'). Based upon  
25 sequence similarity, pw214\_15 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the pw214\_15 protein sequence centered around amino acid 15 of SEQ ID NO:44.

30 Clone "qb56\_19"

A polynucleotide of the present invention has been identified as clone "qb56\_19". qb56\_19 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No.

5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qb56\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qb56\_19 protein").

5       The nucleotide sequence of qb56\_19 as presently determined is reported in SEQ ID NO:45, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qb56\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:46. Amino acids 18 to 40 of SEQ ID NO:46 are a possible leader/signal sequence, with the predicted  
10   mature amino acid sequence beginning at amino acid 41. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the qb56\_19 protein.

      The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
15   qb56\_19 should be approximately 1200 bp.

      The nucleotide sequence disclosed herein for qb56\_19 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qb56\_19 demonstrated at least some similarity with sequences identified as AA632658 (np87c12.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone  
20   IMAGE:1133302), N56430 (JJ8973F Homo sapiens cDNA clone JJ8973 5'), and W05470 (za87f11.r1 Soares fetal lung NbHL19W Homo sapiens cDNA clone 299565 5'). Based upon sequence similarity, qb56\_19 proteins and each similar protein or peptide may share at least some activity.

      qb56\_19 protein was expressed in a COS cell expression system, and an expressed  
25   protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "qc646\_1"

      A polynucleotide of the present invention has been identified as clone "qc646\_1".  
30   qc646\_1 was isolated from a human adult neural tissue (neuroepithelioma HTB-10 line) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded

protein. qc646\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qc646\_1 protein").

The nucleotide sequence of qc646\_1 as presently determined is reported in SEQ ID NO:47, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the qc646\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:48. Amino acids 12 to 24 of SEQ ID NO:48 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 25. Amino acids 32 to 44 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence  
10 beginning at amino acid 45, or are a transmembrane domain. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the qc646\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qc646\_1 should be approximately 1800 bp.

15 The nucleotide sequence disclosed herein for qc646\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qc646\_1 demonstrated at least some similarity with sequences identified as AA470035 (zt94a07.r1 Soares testis NHT Homo sapiens cDNA clone 729972 5'), and AA483957 (ne76e11.s1 NCI\_CGAP\_Ew1 Homo sapiens cDNA clone  
20 IMAGE:910220). The predicted amino acid sequence disclosed herein for qc646\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted qc646\_1 protein demonstrated at least some similarity to sequences identified as D88666 (PS-PLA1 (serine phospholipid-specific phospholipase A) [Rattus norvegicus]), M93284 (lipase related protein 2 [Homo sapiens]),  
25 and R30739 (C-terminally truncated GPL(1-319)), as well as lipases from various other species. Rat PS-PLA1, serine phospholipid-specific phospholipase A, is a member of the lipase family and is secreted from activated platelets. Based upon sequence similarity, qc646\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains  
30 within the qc646\_1 protein sequence, one centered around amino acid 190 and another around amino acid 325 of SEQ ID NO:48. The nucleotide sequence of qc646\_1 indicates that it may contain Alu repetitive elements.



Clone "qf116\_2"

A polynucleotide of the present invention has been identified as clone "qf116\_2". qf116\_2 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf116\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "qf116\_2 protein").

The nucleotide sequence of qf116\_2 as presently determined is reported in SEQ ID NO:49, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf116\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:50.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf116\_2 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for qf116\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. qf116\_2 demonstrated at least some similarity with sequences identified as D50810 (placental leucine aminopeptidase [*Homo sapiens*]), R94512 (GTVap (short version), insulin-cleaving aminopeptidase from GLUT-4 vesicles), and U32990 (vp165 [*Rattus norvegicus*]). Human placental leucine aminopeptidase/oxytocinase (P-LAP), a member of the type II membrane-spanning zinc metallopeptidase family, degrades several peptide hormones such as oxytocin and vasopresin, suggesting a role in maintaining homeostasis during pregnancy. The predicted P-LAP amino acid sequence contains the HEXXH consensus sequence of zinc metallopeptidases, indicating that the enzyme belongs to this family, which includes aminopeptidase N and aminopeptidase A. The deduced P-LAP amino acid sequence also contains a hydrophobic region near the N-terminus, suggesting that the enzyme is a type II integral membrane protein. Results suggest that the enzyme is synthesized as an integral membrane protein and is released into blood under some physiological conditions. (See Røgi *et al.*, 1996, *J. Biol. Chem.* **271**(1): 56-61, which is incorporated by reference herein.) Based upon sequence similarity, qf116\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two potential transmembrane domains within the

qf116\_2 protein sequence, one centered around amino acid 25 and another around amino acid 290 of SEQ ID NO:50.

Clone "qf662\_3"

5 A polynucleotide of the present invention has been identified as clone "qf662\_3". qf662\_3 was isolated from a human adult bladder (carcinoma 5637) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. qf662\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to  
10 herein as "qf662\_3 protein").

The nucleotide sequence of qf662\_3 as presently determined is reported in SEQ ID NO:51, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the qf662\_3 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:52. Amino acids 133 to 145 of SEQ ID NO:52 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 146. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated  
20 from the remainder of the qf662\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone qf662\_3 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for qf662\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
25 FASTA search protocols. qf662\_3 demonstrated no significant similarity with sequences in these databases. The nucleotide sequence of qf662\_3 indicates that it may contain repetitive elements.

Clone "am748\_5"

30 A polynucleotide of the present invention has been identified as clone "am748\_5". am748\_5 was isolated from a human fetal kidney cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. am748\_5 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "am748\_5 protein").

The nucleotide sequence of am748\_5 as presently determined is reported in SEQ ID NO:53, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the am748\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:54. Amino acids 14 to 26 of SEQ ID NO:54 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 27. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the am748\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone am748\_5 should be approximately 1550 bp.

The nucleotide sequence disclosed herein for am748\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. am748\_5 demonstrated at least some similarity with sequences identified as AA418860 (zv98g04.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 767862 5' similar to gb:X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element; contains element PTR5 repetitive element), AC003007 (Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence), H73304 (yu27c10.r1 Homo sapiens cDNA clone 235026 5' similar to contains Alu repetitive element), N35175 (yx83d10.r1 Homo sapiens cDNA clone 268339 5' similar to gb:X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN); contains Alu repetitive element), N41479 (yy05a11.r1 Homo sapiens cDNA clone 270332 5' similar to gb:X14008\_rna1 LYSOZYME C PRECURSOR (HUMAN)), Q81139 (HPLA2-8 gene), T04964 (EST02852 Homo sapiens cDNA clone HFBCI77), and U18391 (Human Alu sequence clone A8). The predicted amino acid sequence disclosed herein for am748\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted am748\_5 protein demonstrated at least some similarity to sequences identified as X55777 (put. ORF [Homo sapiens]) and R13556 (Protein encoded downstream of hhc\_M oncoprotein). Based upon sequence similarity, am748\_5 proteins and each similar protein or peptide may share at least some activity. The nucleotide

sequence of am748\_5 indicates that it may contain one or more of the following repetitive elements: Alu, L1.

Clone "cj507\_1"

5 A polynucleotide of the present invention has been identified as clone "cj507\_1".  
cj507\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj507\_1 is a full-length clone,  
10 including the entire coding sequence of a secreted protein (also referred to herein as "cj507\_1 protein").

The nucleotide sequence of cj507\_1 as presently determined is reported in SEQ ID NO:55, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj507\_1 protein  
15 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:56.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj507\_1 should be approximately 2100 bp.

The nucleotide sequence disclosed herein for cj507\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. cj507\_1 demonstrated at least some similarity with sequences identified as AA100356 (zn46a02.r1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 550442 5' similar to contains element PTR5 repetitive element), AA228100 (zr56g04.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667446 3'), AA479997 (zv18b07.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753973 5' similar to contains  
25 element PTR5 repetitive element, mRNA sequence), and X85324 (H.sapiens mRNA for non polymorphic CAG repeat (CAG12)). Based upon sequence similarity, cj507\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cj507\_1 protein sequence centered around amino acid 265 of SEQ ID NO:56. The  
30 nucleotide sequence of cj507\_1 indicates that it may contain a GCA simple repeat region.

cj507\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 47 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

Clone "cn922\_5"

A polynucleotide of the present invention has been identified as clone "cn922\_5". cn922\_5 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cn922\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cn922\_5 protein").

The nucleotide sequence of cn922\_5 as presently determined is reported in SEQ ID NO:57, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cn922\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:58.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cn922\_5 should be approximately 2200 bp.

The nucleotide sequence disclosed herein for cn922\_5 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cn922\_5 demonstrated at least some similarity with sequences identified as H34191 (EST110864 Rattus sp. cDNA 5' end), R18707 (yf98f02.r1 Homo sapiens cDNA clone 30546 5'), T26556 (Human gene signature HUMGS08801), and Z83230 (Caenorhabditis elegans cosmid F56A8). The predicted amino acid sequence disclosed herein for cn922\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cn922\_5 protein demonstrated at least some similarity to sequences identified as AB004535 (HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION [Schizosaccharomyces pombe]) and Z83230 (F56A8.a and F56A8.1 [Caenorhabditis elegans]). Based upon sequence similarity, cn922\_5 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts six potential transmembrane domains within the cn922\_5 protein sequence, centered around amino acids 25, 100, 135, 190, 290, and 370 of SEQ ID NO:58, respectively. The nucleotide sequence of cn922\_5 indicates that it may contain one or more of the following repetitive elements: MER, L1.

Clone "cw691\_11"

A polynucleotide of the present invention has been identified as clone "cw691\_11". cw691\_11 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw691\_11 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw691\_11 protein").

The nucleotide sequence of cw691\_11 as presently determined is reported in SEQ  
10 ID NO:59, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw691\_11 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:60.

Another potential cw691\_11 reading frame and predicted amino acid sequence is encoded by basepairs 542 to 970 of SEQ ID NO:59 and is reported in SEQ ID NO:179.  
15 Amino acids 34 to 46 of SEQ ID NO:179 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 47. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the protein of SEQ ID NO:179.

20 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw691\_11 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for cw691\_11 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw691\_11 demonstrated at least some similarity with sequences  
25 identified as AA363712 (EST74158 Pancreas I Homo sapiens cDNA 5' end similar to similar to C. elegans hypothetical protein R10E12.1), AA521201 (aa74c10.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone 826674 3'), AA527142 (ni07a10.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE 967290, mRNA sequence), AA745501 (ny64d03.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1283045, mRNA sequence), N73108 (yv69a09.r1 Homo sapiens cDNA clone 247960 5'), T19938 (Human gene signature HUMGS01070), and W77963 (zd70d09.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 346001 5' similar to WP:R10E12.1 CE00310).  
30 The predicted amino acid sequence disclosed herein for cw691\_11 was searched against

the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw691\_11 protein demonstrated at least some similarity to sequences identified as P82971 (Bioadhesive precursor protein from cDNA 52), U73679 (YNK1-a [Caenorhabditis elegans]), and Z29561 (R10E12.1 [Caenorhabditis elegans]).

- 5 Based upon sequence similarity, cw691\_11 proteins and each similar protein or peptide may share at least some activity.

#### Clone "cw1000\_2"

- A polynucleotide of the present invention has been identified as clone "cw1000\_2".
- 10 cw1000\_2 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1000\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein
- 15 as "cw1000\_2 protein").

- The nucleotide sequence of cw1000\_2 as presently determined is reported in SEQ ID NO:61, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1000\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:62. Amino
- 20 acids 24 to 36 of SEQ ID NO:62 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 37. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1000\_2 protein.

- 25 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1000\_2 should be approximately 1500 bp.

- The nucleotide sequence disclosed herein for cw1000\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1000\_2 demonstrated at least some similarity with sequences
- 30 identified as AA446779 (zw89d11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone 784149 5', mRNA sequence), AA493561 (nh04f07.s1 NCI\_CGAP\_Thy1 Homo sapiens cDNA clone 943333 similar to WP:F15G9.4 CE01552 IG SUPERFAMILY REPEATS ;contains element MSR1 repetitive element), H35690 (EST111696 Rattus sp.

1669050: 4490360  
cDNA similar to Opioid binding protein/cell adhesion-like molecule), R18502 (yf96a05.r1  
Homo sapiens cDNA clone 30376 5'), T21582 (Human gene signature HUMGS02965),  
T39504 (ya06g11.r1 Homo sapiens cDNA clone 60740 5'), T46848 (yb94b01.r1 Homo  
sapiens cDNA clone 78793 5'), T51129 (yb94b01.s1 Homo sapiens cDNA clone 78793 3'),  
5 and W67535 (zd40g11.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone  
343172 3' similar to PIR S05539 S05539 glycophorin C - human ;contains element MSR1  
repetitive element). The predicted amino acid sequence disclosed herein for cw1000\_2  
was searched against the GenPept and GeneSeq amino acid sequence databases using the  
BLASTX search protocol. The predicted cw1000\_2 protein demonstrated at least some  
10 similarity to sequences identified as M24406 (poliovirus receptor [Homo sapiens]),  
R07130 (H2OB receptor), W04404 (Human CRTAM; Cytotoxic or Regulatory T-cell  
associated Mol.; CRTAM), X13890 (glycophorin C [Homo sapiens]), and X90569 (elastic  
titin [Homo sapiens]). Based upon sequence similarity, cw1000\_2 proteins and each  
similar protein or peptide may share at least some activity. The TopPredII computer  
15 program predicts an additional potential transmembrane domain within the cw1000\_2  
protein sequence centered around amino acid 358 of SEQ ID NO:62. The nucleotide  
sequence of cw1000\_2 indicates that it may contain a GCC1 repeat element.

20 cw1000\_2 protein was expressed in a COS cell expression system, and an  
expressed protein band of approximately 57 kDa was detected in membrane fractions  
using SDS polyacrylamide gel electrophoresis.

#### Clone "cw1640\_1"

A polynucleotide of the present invention has been identified as clone "cw1640\_1".  
cw1640\_1 was isolated from a human fetal brain cDNA library using methods which are  
25 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
identified as encoding a secreted or transmembrane protein on the basis of computer  
analysis of the amino acid sequence of the encoded protein. cw1640\_1 is a full-length  
clone, including the entire coding sequence of a secreted protein (also referred to herein  
as "cw1640\_1 protein").

30 The nucleotide sequence of cw1640\_1 as presently determined is reported in SEQ  
ID NO:63, and includes a poly(A) tail. What applicants presently believe to be the proper  
reading frame and the predicted amino acid sequence of the cw1640\_1 protein  
corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:64. Amino



acids 123 to 135 of SEQ ID NO:64 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 136. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cw1640\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1640\_1 should be approximately 1400 bp.

The nucleotide sequence disclosed herein for cw1640\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1640\_1 demonstrated at least some similarity with sequences identified as AA075643 (zm88a12.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA clone 544990 5' similar to SW:ACT\_EUPCR P20360 ACTIN), AA411334 (zv29e11.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755084 5' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN ), AA913364 (ol37b07.s1 Soares NFL\_T\_GBC\_S1 Homo sapiens cDNA clone IMAGE:1525621 3' similar to WP:C49H3.8 CE04234 ACTIN-LIKE PROTEIN, mRNA sequence), N25416 (yx40g10.r1 Homo sapiens cDNA clone 264258 5' similar to SP ACT2\_PLAFA P14883 ACTIN), R96887 (yq61g10.r1 Homo sapiens cDNA clone 200322 5'), W37097 (zb98h03.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 5'), W44778 (zb98h03.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320885 3'), W61038 (zc54g09.r1 Soares senescent fibroblasts NbHSF Homo), W76570 (zd66f12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 345647 5' similar to SW:ACT\_PROCL P45521 ACTIN), and W82519 (mf05b01.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone). The predicted amino acid sequence disclosed herein for cw1640\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1640\_1 protein demonstrated at least some similarity to sequences identified as J00068 (alpha-actin [Homo sapiens]), J01163 (actin [Oxytricha fallax]), R22026 (A. chrysogenum actin), R50328 (Drug resistant structural protein), U42436 (Similar to actin-like protein [Caenorhabditis elegans]), and U90439 (actin isolog [Arabidopsis thaliana]). Based upon sequence similarity, cw1640\_1 proteins and each similar protein or peptide may share at least some activity.

Clone "d24\_1"

A polynucleotide of the present invention has been identified as clone "d24\_1". A cDNA clone was first isolated from a human adult blood (peripheral blood mononuclear cells treated with concanavalin A and phorbol myristate acetate) cDNA library using  
5 methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate d24\_1 from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin, phorbol myristate acetate, and mixed lymphocyte  
10 reaction) cDNA library. d24\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "d24\_1 protein").

The nucleotide sequence of d24\_1 as presently determined is reported in SEQ ID NO:65, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the d24\_1 protein corresponding  
15 to the foregoing nucleotide sequence is reported in SEQ ID NO:66. Amino acids 124 to 136 of SEQ ID NO:66 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 137. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the d24\_1  
20 protein. The mRNA sequence encoding amino acids 172 to 175 of SEQ ID NO:66 may not be present in alternatively-spliced forms of d24\_1 mRNA molecules.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone d24\_1 should be approximately 2000 bp.

The nucleotide sequence disclosed herein for d24\_1 was searched against the  
25 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. d24\_1 demonstrated at least some similarity with sequences identified as AA478740 (zv14g12.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 3'), AA479444 (zv14g12.r1 Soares NhHMPu S1 Homo sapiens cDNA clone 753670 5', mRNA sequence), AA278581 (zs76f09.r1 Soares NbHTGBC Homo sapiens  
30 cDNA clone 703433 5' similar to WP T04A8.12 CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), H05202 (yi85h02.r1 Homo sapiens cDNA clone 45213 5' similar to SP T04A8.12m CE01067 YEAST 107.9KD PGK1-MAK32 INTERGENIC HYPOTHETICAL PROTEIN), R74287 (yi57e07.r1 Homo

sapiens cDNA clone 143364 5'), U57715 (*Rattus norvegicus* FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete CDs), and Z35663 (*C. elegans* protein of unknown function). The predicted amino acid sequence disclosed herein for d24\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted d24\_1 protein demonstrated at least some similarity to the sequence identified as U57715 (FGF receptor activating protein FRAG1 [*Rattus norvegicus*]). Lorenzi *et al.* (1996, *Proc. Natl. Acad. Sci. USA* 93:8956, incorporated by reference herein) studied the FRAG1 gene in rat osteosarcoma cells. They concluded that the FRAG1 gene product gets fused to FGF receptor 2 (FGFR2). This fusion "drastically stimulates the transforming activity and autophosphorylation of the receptor" and causes oncogenicity. Based upon sequence similarity, d24\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the d24\_1 protein sequence, centered around amino acids 34, 154, and 194 of SEQ ID NO:66, respectively.

d24\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 24 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "dd426\_1"

A polynucleotide of the present invention has been identified as clone "dd426\_1". A cDNA clone was first isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. This cDNA clone was then used to isolate dd426\_1 from a human adult testes (teratocarcinoma NCCIT) cDNA library. dd426\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd426\_1 protein").

The nucleotide sequence of dd426\_1 as presently determined is reported in SEQ ID NO:67, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd426\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:68. Amino acids 76 to 88 of SEQ ID NO:68 are a predicted leader/signal sequence, with the predicted

666050-FFFF60  
mature amino acid sequence beginning at amino acid 89. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd426\_1 protein.

5           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd426\_1 should be approximately 800 bp.

          The nucleotide sequence disclosed herein for dd426\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd426\_1 demonstrated at least some similarity with sequences  
10 identified as AA760716 (nz13d06.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1287659 similar to WP:F13H10.3 CE05624 YEAST YEH4 LIKE PROTEIN; mRNA sequence), H11919 (ym10e10.r1 Homo sapiens cDNA clone 47462 5'), and Z68748 (Caenorhabditis elegans cosmid F13H10). The predicted amino acid sequence disclosed herein for dd426\_1 was searched against the GenPept and GeneSeq amino acid  
15 sequence databases using the BLASTX search protocol. The predicted dd426\_1 protein demonstrated at least some similarity to sequences identified as U39782 (lysine and histidine specific transporter [Arabidopsis thaliana]) and Z68748 (F13H10.3 [Caenorhabditis elegans]). Based upon sequence similarity, dd426\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program  
20 predicts an additional potential transmembrane domain within the dd426\_1 protein sequence centered around amino acid 30 of SEQ ID NO:68, which may also function as a leader/signal sequence.

          dd426\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 12 kDa was detected in membrane fractions using SDS  
25 polyacrylamide gel electrophoresis.

#### Clone "di393\_2"

          A polynucleotide of the present invention has been identified as clone "di393\_2". di393\_2 was isolated from a human adult testes cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. di393\_2 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "di393\_2 protein").

The nucleotide sequence of di393\_2 as presently determined is reported in SEQ ID NO:69, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the di393\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:70. Amino acids 7 to 19 of SEQ ID NO:70 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain  
10 should the predicted leader/signal sequence not be separated from the remainder of the di393\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone di393\_2 should be approximately 600 bp.

The nucleotide sequence disclosed herein for di393\_2 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. di393\_2 demonstrated at least some similarity with sequences identified as AA669506 (zu85g08.s1 Soares testis NHT Homo sapiens cDNA clone 744830 3', mRNA sequence). Based upon sequence similarity, di393\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer  
20 program predicts an additional potential transmembrane domain within the di393\_2 protein sequence centered around amino acid 66 of SEQ ID NO:70.

di393\_2 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 20 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

25

#### Clone "dj167\_2"

A polynucleotide of the present invention has been identified as clone "dj167\_2". dj167\_2 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167\_2 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_2 protein").

The nucleotide sequence of dj167\_2 as presently determined is reported in SEQ ID NO:71, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:72.

5       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_2 should be approximately 1550 bp.

10       The nucleotide sequence disclosed herein for dj167\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dj167\_2 demonstrated at least some similarity with sequences identified as H49161 (yq18d05.r1 Soares fetal liver spleen 1NFLS Homo sapiens cDNA clone 274208 5'), L12350 (Human thrombospondin 2 (THBS2) mRNA, complete cds), T98917 (ye66b03.s1 Homo sapiens cDNA clone 122669 3' similar to SP:TSP1\_CHICK P35440 THROMBOSPONDIN 1), and X87620 (B.taurus mRNA for complete thrombospondin). The predicted amino acid sequence disclosed herein for dj167\_2 was  
15       searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dj167\_2 protein demonstrated at least some similarity to sequences identified as L12350 (thrombospondin 2 [Homo sapiens]), M60853 (thrombospondin [Gallus gallus]), R40823 (Human thrombospondin 1), U48245 (protein kinase C-binding protein Nel [Rattus norvegicus]), X87620 (thrombospondin [Bos  
20       taurus]), and Z71178 (B0024.14 [Caenorhabditis elegans]). Based upon sequence similarity, dj167\_2 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three potential transmembrane domains within the dj167\_2 protein sequence, centered around amino acids 140, 215, and 315 of SEQ ID NO:72, respectively.

25

#### Clone "dj167\_19"

A polynucleotide of the present invention has been identified as clone "dj167\_19". dj167\_19 was isolated from a human adult placenta cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30       identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dj167\_19 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dj167\_19 protein").

5 The nucleotide sequence of dj167\_19 as presently determined is reported in SEQ ID NO:73, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dj167\_19 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:74. Amino acids 22 to 34 of SEQ ID NO:74 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 35. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dj167\_19 protein. The dj167\_19 clone is related to that of dj167\_2, and extends further 5'.  
10 The dj167\_19 clone appears to contain coding sequences for chorionic somatomammotropin in the opposite orientation at its 5' end between Sfi restriction sites (at nucleotides 16 and 839 of SEQ ID NO:73). The dj167\_2 and dj167\_19 clones may represent alternatively spliced messenger RNA molecules encoding two different forms of a secreted protein.

15 The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dj167\_19 should be approximately 4500 bp.

Analysis of the dj167\_19 amino acid sequence (SEQ ID NO:74) reveals the following domains: IGFBP cysteine-rich domain at amino acids 60-75; VWF-B cysteine-rich domains at amino acids 174-210, 212-247, 255-291, and 293-328; Chordin cysteine-rich domains at amino acids 336-390, 403-456, 608-662, 679-734, 753-808, and 819-873;  
20 Antistatin (protease inhibitor) cysteine-rich domains at amino acids 469-498, 505-532, 539-564, and 567-592; RGD cell attachment sequence at amino acids 314-316, and Asn glycosylation sites at amino acids 71, 113, 330, 474, and 746. The cysteine-rich domains listed above are similar to domains found in the C domain of Von Willebrand Factor (VWF), and in procollagen and thrombospondin. In addition, the amino acid sequence  
25 of SEQ ID NO:74 from amino acid 938 to amino acid 960 appears to be a transmembrane domain.

The dj167\_19 transcript is expressed in several cell types, including kidney, pancreas, spleen, and ovary, and is most abundantly expressed in placental tissue.

30

#### Clone "dw665\_4"

A polynucleotide of the present invention has been identified as clone "dw665\_4". dw665\_4 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was

identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dw665\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dw665\_4 protein").

5           The nucleotide sequence of dw665\_4 as presently determined is reported in SEQ ID NO:75, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dw665\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:76. Amino acids 15 to 27 of SEQ ID NO:76 are a predicted leader/signal sequence, with the predicted  
10   mature amino acid sequence beginning at amino acid 28. Amino acids 16 to 28 of SEQ ID NO:76 are also a predicted leader/signal sequence, with the predicted mature amino acid sequence in that case beginning at amino acid 29. Due to the hydrophobic nature of these predicted leader/signal sequences, each is likely to act as a transmembrane domain should it not be separated from the remainder of the dw665\_4 protein.

15           The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dw665\_4 should be approximately 3750 bp.

          The nucleotide sequence disclosed herein for dw665\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dw665\_4 demonstrated at least some similarity with sequences  
20   identified as AA029053 (zk09f06.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 470051 3'), H77289 (EST27o17 WATM1 Homo sapiens cDNA clone 27o17, mRNA sequence), and T21722 (Human gene signature HUMGS03170). The predicted amino acid sequence disclosed herein for dw665\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
25   dw665\_4 protein demonstrated at least some similarity to sequences identified as L35764 (chordin [*Xenopus laevis*]) and W31559 (*Xenopus* frog protein "chordin"). Analysis of motifs within the predicted dw665\_4 protein revealed the presence of Chordin cysteine-rich domains at amino acids 37-99, 115-178, and 260-322 of SEQ ID NO:76; an 'RGD' cell-attachment sequence (at amino acids 179-181 of SEQ ID NO:76), which in some  
30   proteins has been shown to play a role in cell adhesion; and Asp glycosylation sites at amino acids 118 and 291. Based upon sequence similarity, dw665\_4 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of dw665\_4 indicates that it may contain an AC repetitive element.



dw665\_4 transcripts are expressed in many tissues including kidney, adrenal gland, and prostate tissues, and are most abundantly expressed in pancreas; however, little or no dw665\_4 transcript expression is observed in liver or peripheral blood cells. dw665\_4 protein was expressed in a COS cell expression system, and an expressed  
5 protein band of approximately 75 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis; two additional bands at approximately 26 and 30 kDa were also observed. BIACORE binding experiments indicate that dw665\_4 protein has a Chordin-like protein-binding profile, and binds to BMP-2, BMP-4, BMP-7, BMP-12, and GDF-5.

10 Clone "dx146\_12"

A polynucleotide of the present invention has been identified as clone "dx146\_12". dx146\_12 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
15 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx146\_12 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx146\_12 protein").

The nucleotide sequence of dx146\_12 as presently determined is reported in SEQ  
20 ID NO:77, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dx146\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:78.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx146\_12 should be approximately 2250 bp.

25 The nucleotide sequence disclosed herein for dx146\_12 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx146\_12 demonstrated at least some similarity with sequences identified as AA090429 (y0527.seq.F Fetal heart, Lambda ZAP Express Homo sapiens cDNA 5'), AA232068 (zr24a01.r1 Stratagene NT2 neuronal precursor 937230 Homo sapiens cDNA clone 664296 5'), AA886679 (oj47h07.s1 NCI\_CGAP\_Kid3 Homo sapiens  
30 cDNA clone IMAGE:1501501 3' similar to WP:F16A11.2 CE09424 METHANOCOCCUS HYPOTHETICAL PROTEIN 0682 LIKE; mRNA sequence), R61436 (yh15g06.r1 Homo sapiens cDNA clone 37884 5'), and Z81505 (Caenorhabditis elegans

cosmid F16A11, complete sequence). The predicted amino acid sequence disclosed herein for dx146\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted dx146\_12 protein demonstrated at least some similarity to sequences identified as U67515 (hypothetical protein (SP P46850) [Methanococcus jannaschii]) and Z81505 (F16A11.2 [Caenorhabditis elegans]). Based upon sequence similarity, dx146\_12 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the dx146\_12 protein sequence centered around amino acid 405 of SEQ ID NO:78.

dx146\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 50 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "dx219\_13"

A polynucleotide of the present invention has been identified as clone "dx219\_13". dx219\_13 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dx219\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dx219\_13 protein").

The nucleotide sequence of dx219\_13 as presently determined is reported in SEQ ID NO:79, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dx219\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:80. Amino acids 94 to 106 of SEQ ID NO:80 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 107. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dx219\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dx219\_13 should be approximately 1200 bp.

The nucleotide sequence disclosed herein for dx219\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dx219\_13 demonstrated at least some similarity with sequences identified as AA429731 (zw66g05.s1 Soares testis NHT Homo sapiens cDNA clone 781208 3'), AA446067 (zw66e06.r1 Soares testis NHT Homo sapiens cDNA clone 781186 5', mRNA sequence), T23212 (standard; cDNA to mRNA; 161 BP, Human gene signature HUMGS05005), W29299 (mb99f03.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 337565 5'), W87852 (zh68b05.r1 Soares fetal liver spleen 1NFLS S1 Homo sapiens cDNA clone 417201 5'), and Y13897 (Homo sapiens partial mRNA for hypothetical protein). Based upon sequence similarity, dx219\_13 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the dx219\_13 protein sequence, one centered around amino acid 160 and another around amino acid 275 of SEQ ID NO:80.

dx219\_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 37 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "fm3\_1"

A polynucleotide of the present invention has been identified as clone "fm3\_1". fm3\_1 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. fm3\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "fm3\_1 protein").

The nucleotide sequence of fm3\_1 as presently determined is reported in SEQ ID NO:81, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the fm3\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:82. Amino acids 7 to 19 of SEQ ID NO:82 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 20. Due to the hydrophobic nature of the

predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the fm3\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone  
5 fm3\_1 should be approximately 600 bp.

The nucleotide sequence disclosed herein for fm3\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. fm3\_1 demonstrated at least some similarity with sequences identified as T15669 (IB1718 Infant brain, Bento Soares Homo sapiens cDNA 3'end).  
10 Based upon sequence similarity, fm3\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domains within the fm3\_1 protein sequence centered around amino acid 85 of SEQ ID NO:82.

fm3\_1 protein was expressed in a COS cell expression system, and an expressed  
15 protein band of approximately 9 kDa was detected in membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "h225\_1"

A polynucleotide of the present invention has been identified as clone "h225\_1".  
20 h225\_1 was isolated from a human adult blood (peripheral blood mononuclear cells treated with phytohemagglutinin and phorbol myristate acetate and mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of  
25 the encoded protein. h225\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "h225\_1 protein").

The nucleotide sequence of h225\_1 as presently determined is reported in SEQ ID NO:83. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the h225\_1 protein corresponding to the foregoing  
30 nucleotide sequence is reported in SEQ ID NO:84. Amino acids 52 to 64 of SEQ ID NO:84 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 65. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the h225\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone h225\_1 should be approximately 832 bp.

The nucleotide sequence disclosed herein for h225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. h225\_1 demonstrated at least some similarity with sequences identified as AA604374 (no87e01.s1 NCI\_CGAP\_AA1 Homo sapiens cDNA clone IMAGE:1113816 similar to WP:ZK757.1 CE00467; mRNA sequence), H18393 (yn49a12.r1 Homo sapiens cDNA clone 171742 5' similar to SP:ZK757.1 CE00467), and R23642 (yh35e03.r1 Homo sapiens cDNA clone 131740 5'). The predicted amino acid sequence disclosed herein for h225\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted h225\_1 protein demonstrated at least some similarity to sequences identified as AL022600 (hypothetical protein [Schizosaccharomyces pombe]) and Z48758 (SC9727\_21 unknown [Saccharomyces cerevisiae]). Based upon sequence similarity, h225\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "kj320\_1"

A polynucleotide of the present invention has been identified as clone "kj320\_1". kj320\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. kj320\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "kj320\_1 protein").

The nucleotide sequence of kj320\_1 as presently determined is reported in SEQ ID NO:85, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the kj320\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:86. Amino acids 26 to 38 of SEQ ID NO:86 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 39. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the kj320\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone kj320\_1 should be approximately 4900 bp.

The nucleotide sequence disclosed herein for kj320\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. kj320\_1 demonstrated at least some similarity with sequences identified as A45343 (Sequence 13 from Patent WO9517522), AA284111 (zc36f08.T7 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 324423 3' similar to WP ZK688.8 CE00544 UDP-GALNAC; mRNA sequence), AA375707 (EST88026 HSC172 cells II Homo sapiens cDNA 5' end), AA534406 (nf76b08.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE 925815), D39885 (Rice cDNA, partial sequence (S1531\_1A)), G10010 (human STS CHLC.GCT16E06.P18287 clone GCT16E06), Q75104 (Cattle GalNAc-transferase), Q95187 (Simple tandem repeat (STR) corresponding to wg1d10), and U35890 (Rattus norvegicus polypeptide GalNAc transferase T1 mRNA, complete cds). The predicted amino acid sequence disclosed herein for kj320\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted kj320\_1 protein demonstrated at least some similarity to sequences identified as R66397 (Cattle GalNAc-transferase), U41514 (UDP-GalNAc polypeptide N-acetylgalactosaminyltransferase [Homo sapiens]), and X85018 (UDP-GalNAc polypeptide N-acetylgalactosaminyl transferase [Homo sapiens]). Analysis of motifs within kj320\_1 reveals the presence of the alpha-2-macroglobulin family thiolester region signature. The proteinase-binding alpha-macroglobulins (A2M) are large glycoproteins found in the plasma of vertebrates, in the hemolymph of some invertebrates, and in reptilian and avian egg white. They inhibit all four classes of proteinases by trapping a proteinase with a peptide stretch containing the specific cleavage site (the 'bait' region) which upon proteinase binding induces a conformational change in the protein, trapping the proteinase. Upon cleavage of the 'bait' region, a covalent bond (a thiol-ester bond between the side chains of a cysteine and a glutamine) is formed between the A2M and the proteinase. Based upon sequence similarity, kj320\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of kj320\_1 indicates that it may contain one or more repetitive elements.

kj320\_1 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 136 kDa was detected in conditioned medium using SDS polyacrylamide gel electrophoresis.

5        Clone "ml236\_5"

A polynucleotide of the present invention has been identified as clone "ml236\_5". ml236\_5 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
10       analysis of the amino acid sequence of the encoded protein. ml236\_5 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml236\_5 protein").

The nucleotide sequence of ml236\_5 as presently determined is reported in SEQ ID NO:87, and includes a poly(A) tail. What applicants presently believe to be the proper  
15       reading frame and the predicted amino acid sequence of the ml236\_5 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:88. Amino acids 148 to 160 of SEQ ID NO:88 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 161. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
20       transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml236\_5 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml236\_5 should be approximately 1300 bp.

The nucleotide sequence disclosed herein for ml236\_5 was searched against the  
25       GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml236\_5 demonstrated at least some similarity with sequences identified as AA137204 (zl23h11.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 502821 3'), AA307966 (EST17887 Aorta endothelial cells, TNF alpha-treated Homo sapiens cDNA 5' end, mRNA sequence), AA434504 (zw31c03.r1 Soares ovary tumor  
30       NbHOT Homo sapiens cDNA clone 770884 5' similar to WP C45G9.7 CE01858), AA525971 (ni93g09.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone 984448), AA526490 (ni96c11.s1 NCI\_CGAP\_Pr21 Homo sapiens cDNA clone IMAGE 984692, mRNA sequence), AF028823 (Homo sapiens Tax interaction protein 1 mRNA, partial

cds), U90913 (Human clone 23665 mRNA sequence), and W73114 (zd55c12.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 344566 5'). The predicted amino acid sequence disclosed herein for ml236\_5 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted  
5 ml236\_5 protein demonstrated at least some similarity to sequences identified as AF028823 (Tax interaction protein 1 [Homo sapiens]) and U21323 (similar to tight junction protein (ZO-1) (SP Z01\_HUMAN, Q07157) [Caenorhabditis elegans]). Based upon sequence similarity, ml236\_5 proteins and each similar protein or peptide may share at least some activity.

10 ml236\_5 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 14 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "pu282\_10"

15 A polynucleotide of the present invention has been identified as clone "pu282\_10". pu282\_10 was isolated from a human adult blood (promyelocytic leukemia HL-60) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein.  
20 pu282\_10 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "pu282\_10 protein").

The nucleotide sequence of pu282\_10 as presently determined is reported in SEQ ID NO:89, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the pu282\_10 protein  
25 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:90. Amino acids 119 to 131 of SEQ ID NO:90 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 132. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated  
30 from the remainder of the pu282\_10 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone pu282\_10 should be approximately 1050 bp.



5 The nucleotide sequence disclosed herein for pu282\_10 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. pu282\_10 demonstrated at least some similarity with sequences identified as AA311503 (EST182442 Jurkat T-cells VI Homo sapiens cDNA 5' end),  
10 AA336709 (EST41341 Endometrial tumor Homo sapiens cDNA 5' end), AA336890 (EST41572 Endometrial tumor), AA385588 (EST99290 Thyroid Homo sapiens cDNA 5' end), AA526889 (ni09e05.s1 NCI\_CGAP\_Br2 Homo sapiens cDNA clone IMAGE:967520), AC003058 (Arabidopsis thaliana "unknown" protein), and T19726 (Human gene signature HUMGS00800). Based upon sequence similarity, pu282\_10 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the pu282\_10 protein sequence, one centered around amino acid 39 and another around amino acid 95 of SEQ ID NO:90.

15 pu282\_10 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 16 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "at94\_2"

20 A polynucleotide of the present invention has been identified as clone "at94\_2". at94\_2 was isolated from a human adult blood (lymphocytes and dendritic cells treated with mixed lymphocyte reaction) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. at94\_2 is a full-length clone, including the  
25 entire coding sequence of a secreted protein (also referred to herein as "at94\_2 protein").

The nucleotide sequence of at94\_2 as presently determined is reported in SEQ ID NO:91, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the at94\_2 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:92. Amino acids 214 to  
30 226 of SEQ ID NO:92 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 227. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should

the predicted leader/signal sequence not be separated from the remainder of the at94\_2 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone at94\_2 should be approximately 4300 bp.

5        The nucleotide sequence disclosed herein for at94\_2 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. at94\_2 demonstrated at least some similarity with sequences identified as N24317 (yx23d12.r1 Homo sapiens cDNA clone 262583 5'), T30988 (EST25695 Homo sapiens cDNA 5' end similar to None), and U37026 (Rattus norvegicus  
10 brain sodium channel beta 2 subunit (SCNB2) mRNA, complete cds). The predicted amino acid sequence disclosed herein for at94\_2 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted at94\_2 protein demonstrated at least some similarity to the sequence identified as Z49912 (T24F1.2 [Caenorhabditis elegans]). Based upon sequence similarity, at94\_2 proteins and  
15 each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the at94\_2 protein sequence, centered around amino acids 23, 306, 332, and 364 of SEQ ID NO:92, respectively.

20        Clone "bf169\_13"

A polynucleotide of the present invention has been identified as clone "bf169\_13". bf169\_13 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer  
25 analysis of the amino acid sequence of the encoded protein. bf169\_13 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "bf169\_13 protein").

The nucleotide sequence of bf169\_13 as presently determined is reported in SEQ ID NO:93, and includes a poly(A) tail. What applicants presently believe to be the proper  
30 reading frame and the predicted amino acid sequence of the bf169\_13 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:94. Amino acids 342 to 354 are a possible leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 355. Due to the hydrophobic nature of this

possible leader/signal sequence, it is likely to act as a transmembrane domain should it not be separated from the remainder of the bf169\_13 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bf169\_13 should be approximately 3000 bp.

5        The nucleotide sequence disclosed herein for bf169\_13 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bf169\_13 demonstrated at least some similarity with sequences identified as AA227952 (zr56b06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 667379 3'), AA453914 (zx32e11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA  
10   clone 788204 5' similar to contains element TAR1 repetitive element; mRNA sequence), H46157 (yo13f11.r1 Homo sapiens cDNA clone 177837 5'), H18792 (yn52e02.r1 Homo sapiens cDNA clone 172058 5'), and N24601 (yx72e01.s1 Homo sapiens cDNA clone 267288 3'). The predicted amino acid sequence disclosed herein for bf169\_13 was searched against the GenPept and GeneSeq amino acid sequence databases using the  
15   BLASTX search protocol. The predicted bf169\_13 protein demonstrated at least some similarity to sequences identified as L41834 (plant nuclear protein [Ensis minor]) and Z75539 (F28C1.1 [Caenorhabditis elegans]). Analysis of motifs in the predicted bf169\_13 protein revealed a "mitochondrial energy transfer proteins" signature at amino acid 574 of SEQ ID NO:94. Based upon sequence similarity, bf169\_13 proteins and each similar  
20   protein or peptide may share at least some activity. The nucleotide sequence of bf169\_13 indicates that it may contain one or more GCCCCA, GCCC, GGA and/or GC repeat sequences.

      bf169\_13 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 109 kDa was detected in membrane fractions  
25   using SDS polyacrylamide gel electrophoresis.

#### Clone "bl152\_12"

      A polynucleotide of the present invention has been identified as clone "bl152\_12". bl152\_12 was isolated from a human adult testes cDNA library using methods which are  
30   selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. bl152\_12 is a full-length

clone, including the entire coding sequence of a secreted protein (also referred to herein as "bl152\_12 protein").

The nucleotide sequence of bl152\_12 as presently determined is reported in SEQ ID NO:95, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the bl152\_12 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:96.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bl152\_12 should be approximately 1100 bp.

The nucleotide sequence disclosed herein for bl152\_12 was searched against the  
10 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. bl152\_12 demonstrated at least some similarity with sequences identified as AA280876 (zs97d04.s1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559 3' similar to contains element MER22 repetitive element), AA280956 (zs97d04.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone 711559  
15 5'), R21512 (yh19b03.s1 Homo sapiens cDNA clone 130157 3'), R67018 (yi26e05.s1 Homo sapiens cDNA clone 140384 3' similar to contains MER22 repetitive element), R71877 (yj87d11.s1 Homo sapiens cDNA clone 155733 3' similar to contains MER22 repetitive element), T22941 (Human gene signature HUMGS04666), W46539 (zc30g03.s1 Soares senescent fibroblasts NbHSF Homo sapiens cDNA clone 323860 3', mRNA  
20 sequence), and W70065 (zd49c04.s1 Soares fetal heart NbHH19W Homo sapiens cDNA clone). The predicted amino acid sequence disclosed herein for bl152\_12 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted bl152\_12 protein demonstrated at least some similarity to the sequence identified as Z82256 (B0513.2 [Caenorhabditis elegans]). Based upon  
25 sequence similarity, bl152\_12 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bl152\_12 indicates that it may contain one or more GCC repeat sequences.

bl152\_12 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 25 kDa was detected in conditioned medium using SDS  
30 polyacrylamide gel electrophoresis.

Clone "bz578\_1"

A polynucleotide of the present invention has been identified as clone "bz578\_1". bz578\_1 was isolated from a human fetal kidney cDNA library using methods and was identified as encoding a novel protein on the basis of computer analysis of the amino acid  
5 sequence of the encoded protein. bz578\_1 is a full-length clone, including the entire coding sequence of a novel protein (also referred to herein as "bz578\_1 protein").

The nucleotide sequence of bz578\_1 as presently determined is reported in SEQ ID NO:97, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the bz578\_1 protein  
10 corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:98.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone bz578\_1 should be approximately 1000 bp.

The nucleotide sequence disclosed herein for bz578\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
15 FASTA search protocols. bz578\_1 demonstrated at least some similarity with sequences identified as T47038 (yb12e08.r1 Homo sapiens cDNA clone 70982 5' contains L1 repetitive element) and Z82975 (Human DNA sequence from PAC 36J3, between markers DXS1192 and DXS102 on chromosome X). The predicted amino acid sequence disclosed herein for bz578\_1 was searched against the GenPept and GeneSeq amino acid sequence  
20 databases using the BLASTX search protocol. The predicted bz578\_1 protein demonstrated at least some similarity to sequences identified as AF051782 (diaphanous 1 [Homo sapiens]), U96963 (diaphanous 1 [mouse]), and U93572 (putative p150 [Homo sapiens]). Based upon sequence similarity, bz578\_1 proteins and each similar protein or peptide may share at least some activity. The nucleotide sequence of bz578\_1 indicates  
25 that it may contain one or more L1 repeat sequences.

Clone "cb123\_1"

A polynucleotide of the present invention has been identified as clone "cb123\_1". cb123\_1 was isolated from a human fetal brain cDNA library using methods which are  
30 selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cb123\_1 is a full-length clone,

including the entire coding sequence of a secreted protein (also referred to herein as "cb123\_1 protein").

The nucleotide sequence of cb123\_1 as presently determined is reported in SEQ ID NO:99, and includes a poly(A) tail. What applicants presently believe to be the proper  
5 reading frame and the predicted amino acid sequence of the cb123\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:100. Amino acids 44 to 56 of SEQ ID NO:100 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 57. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a  
10 transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the cb123\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cb123\_1 should be approximately 1500 bp.

The nucleotide sequence disclosed herein for cb123\_1 was searched against the  
15 GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cb123\_1 demonstrated at least some similarity with sequences identified as AA309020 (EST179803 Colon carcinoma (Caco-2) cell line I Homo sapiens cDNA 5' end, mRNA sequence), R89617 (ym98b08.s1 Homo sapiens cDNA clone 166935 3'), T16814 (NIB1893 Normalized infant brain, Bento Soares Homo sapiens cDNA 3'end  
20 similar to EST02882 H. sapiens cDNA clone HFBCL71), T24092 (Human gene signature HUMGS06080), and T55187 (yb43e06.s1 Homo sapiens cDNA clone 73954 3'). The predicted amino acid sequence disclosed herein for cb123\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cb123\_1 protein demonstrated at least some similarity to the sequence  
25 identified as U33331 (orf UL133 [Human cytomegalovirus]). Based upon sequence similarity, cb123\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts two additional potential transmembrane domains within the cb123\_1 protein sequence, one centered around amino acid 15 and another around amino acid 80 of SEQ ID NO:100.

30

#### Clone "ch245\_1"

A polynucleotide of the present invention has been identified as clone "ch245\_1". ch245\_1 was isolated from a human fetal kidney cDNA library using methods which are

selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ch245\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as  
5 "ch245\_1 protein").

The nucleotide sequence of ch245\_1 as presently determined is reported in SEQ ID NO:101, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ch245\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:102. The  
10 TopPredII computer program predicts a potential transmembrane domain within the ch245\_1 protein sequence centered around amino acid 87 of SEQ ID NO:102.

Another potential ch245\_1 reading frame and predicted amino acid sequence is encoded by basepairs 533 to 778 of SEQ ID NO:101 and is reported in SEQ ID NO:180. The TopPredII computer program predicts a potential transmembrane domain within the  
15 SEQ ID NO:180 amino acid sequence centered around amino acid 34 of SEQ ID NO:180.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ch245\_1 should be approximately 1350 bp.

The nucleotide sequence disclosed herein for ch245\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and  
20 FASTA search protocols. ch245\_1 demonstrated at least some similarity with sequences identified as AA402307 (zu48f03.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 741245 5', mRNA sequence), H19032 (ym44e04.r1 Homo sapiens cDNA clone 50921 5'), H19323 (ym44e04.s1 Homo sapiens cDNA clone 50921 3'), and N36070 (yy02g11.r1 Homo sapiens cDNA clone 270116 5'). The predicted amino acid sequence  
25 disclosed herein for ch245\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ch245\_1 protein demonstrated at least some similarity to the sequence identified as M58597 (ELAM-1 ligand fucosyltransferase [Homo sapiens]) and U36763 (fatty acid synthase [Mycobacterium bovis]). Based upon sequence similarity, ch245\_1 proteins and each  
30 similar protein or peptide may share at least some activity.

Clone "cj378\_3"

A polynucleotide of the present invention has been identified as clone "cj378\_3". cj378\_3 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cj378\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cj378\_3 protein").

The nucleotide sequence of cj378\_3 as presently determined is reported in SEQ ID  
10 NO:103, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cj378\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:104.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cj378\_3 should be approximately 1400 bp.

15 The nucleotide sequence disclosed herein for cj378\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cj378\_3 demonstrated at least some similarity with sequences identified as D60138 (Human fetal brain cDNA 5'-end GEN-088A04, mRNA sequence), H19318 (ym44d06.s1 Homo sapiens cDNA clone 51231 3'), H41859 (yo07g06.r1 Homo  
20 sapiens cDNA clone 177274 5'), T25386 (Human gene signature HUMGS07551), and T75383 (yc89g05.r1 Homo sapiens cDNA clone 23351 5'). Based upon sequence similarity, cj378\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain at the N-terminus of the the cj378\_3 protein sequence (SEQ ID NO:104).

25

Clone "cw1481\_1"

A polynucleotide of the present invention has been identified as clone "cw1481\_1". cw1481\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
30 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. cw1481\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "cw1481\_1 protein").



The nucleotide sequence of cw1481\_1 as presently determined is reported in SEQ ID NO:105, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the cw1481\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:106.

5       The EcoRI/NotI restriction fragment obtainable from the deposit containing clone cw1481\_1 should be approximately 2380 bp.

10       The nucleotide sequence disclosed herein for cw1481\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. cw1481\_1 demonstrated at least some similarity with sequences identified as AA027927 (zk05a10.r1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 5'), AA027928 (zk05a10.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 469626 3' similar to contains MER28.b2 MER28 repetitive element), AA113357 (zn69g06.s1 Stratagene HeLa cell s3 937216 Homo sapiens cDNA clone 563482 3'), AA252304 (zs12b08.s1 Soares NbHTGBC Homo sapiens cDNA clone 684951 3' similar to contains element MER22 repetitive element), AA976744 (oq09a09.s1 NCI\_CGAP\_GC4 Homo sapiens cDNA clone IMAGE 1585816 3' similar to TR O15025 O15025 KIAA0308 ;contains element MER22 repetitive element; mRNA sequence), R55084 (yg87a06.r1 Homo sapiens cDNA clone 40244 5'), U00930 (Human clone C4E 1.63 (CAC)n/(GTG)n repeat-containing mRNA), U00955 (Human clone CE29 8.1 20 (CAC)n/(GTG)n repeat-containing mRNA), and W16808 (zb93a09.s1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 320344 3'). The predicted amino acid sequence disclosed herein for cw1481\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted cw1481\_1 protein demonstrated at least some similarity to sequences identified as AB002306 (KIAA0308 25 [Homo sapiens]), X15906 (precursor polypeptide), and Z68751 (F01G4.1 [Caenorhabditis elegans]). Based upon sequence similarity, cw1481\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the cw1481\_1 protein sequence centered around amino acid 431 of SEQ ID NO:106, and a putative transmembrane domain within the 30 cw1481\_1 protein sequence centered around amino acid 395 of SEQ ID NO:106. The amino acid sequence of cw1481\_1 indicates that it has a histidine-rich region and a serine-rich region, and it is strongly internally repeated.

Clone "dd119\_4"

A polynucleotide of the present invention has been identified as clone "dd119\_4". dd119\_4 was isolated from a human adult testes cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was  
5 identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. dd119\_4 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "dd119\_4 protein").

The nucleotide sequence of dd119\_4 as presently determined is reported in SEQ  
10 ID NO:107, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the dd119\_4 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:108. Amino acids 27 to 39 of SEQ ID NO:108 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 40. Due to the  
15 hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the dd119\_4 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone dd119\_4 should be approximately 3350 bp.

20 The nucleotide sequence disclosed herein for dd119\_4 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. dd119\_4 demonstrated at least some similarity with sequences identified as AA151924 (zo30e05.r1 Stratagene colon (#937204) Homo sapiens cDNA clone 588416 5' similar to SW SLIT\_DROME P24014 SLIT PROTEIN PRECURSOR;  
25 mRNA sequence), AA193464 (zr41c06.s1 Soares NhHMPu S1 Homo sapiens cDNA clone 665962 3'), AB011135 (Homo sapiens mRNA for KIAA0563 protein, complete cds), G23888 (human STS WI-12393), H04996 (yl74c12.s1 Homo sapiens cDNA clone 43851 3'), M86526 (Rat proline-rich protein (PRP) gene, 5' end, and containing several Alu-like repetitive elements), M86514 (Rat proline-rich protein mRNA, 3' end), W68823  
30 (zd37f04.r1 Soares fetal heart NbHH19W Homo sapiens cDNA clone 342847 5'), and Z54386 (H.sapiens CpG island DNA genomic MseI fragment, clone 10g3, forward read cpg10g3.ft1a). The predicted amino acid sequence disclosed herein for dd119\_4 was searched against the GenPept and GeneSeq amino acid sequence databases using the

BLASTX search protocol. The predicted dd119\_4 protein demonstrated at least some similarity to sequences identified as AB011135 (KIAA0563 protein [Homo sapiens]) and M86526 (proline-rich protein [Rattus norvegicus]). The rat proline-rich protein (PRP) is encoded by a single-copy gene and is expressed in the ventral prostate of the rat, with the precursor protein product being cleaved into multiple proline-rich polypeptides. Based upon sequence similarity, dd119\_4 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the dd119\_4 protein sequence centered around amino acid 928 of SEQ ID NO:108.

dd119\_4 protein was expressed in a COS cell expression system, and an expressed protein band of approximately 166 kDa was detected in conditioned medium and membrane fractions using SDS polyacrylamide gel electrophoresis.

#### Clone "df202\_3"

A polynucleotide of the present invention has been identified as clone "df202\_3". df202\_3 was isolated from a human adult brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. df202\_3 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "df202\_3 protein").

The nucleotide sequence of df202\_3 as presently determined is reported in SEQ ID NO:109, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the df202\_3 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:110. Amino acids 17 to 29 of SEQ ID NO:110 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 30. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the df202\_3 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone df202\_3 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for df202\_3 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and

FASTA search protocols. df202\_3 demonstrated at least some similarity with sequences identified as AA138679 (mq76g03.r1 Stratagene mouse melanoma (#937312) Mus musculus cDNA clone 584692 5'), AA283121 (zt17b05.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 713361 3'), AA286996 (zs58c10.r1 NCI\_CGAP\_GCB1 Soares NbHTGBC Homo sapiens cDNA clone IMAGE 701682 5'), N54968 (yv38g01.s1 Homo sapiens cDNA clone 245040 3'), T20071 (Human gene signature HUMGS01213), and W28275 (44g12 Human retina cDNA randomly primed sublibrary Homo sapiens cDNA). The predicted amino acid sequence disclosed herein for df202\_3 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol.

10 The predicted df202\_3 protein demonstrated at least some similarity to the sequence identified as Z81137 (W02D9.h [Caenorhabditis elegans]). Based upon sequence similarity, df202\_3 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts three additional potential transmembrane domains within the df202\_3 protein sequence, centered around amino

15 acids 55, 80, and 108 of SEQ ID NO:110, respectively.

#### Clone "km225\_1"

A polynucleotide of the present invention has been identified as clone "km225\_1". km225\_1 was isolated from a human adult retina cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. km225\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "km225\_1 protein").

20

25 The nucleotide sequence of km225\_1 as presently determined is reported in SEQ ID NO:111, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the km225\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:112. Amino acids 9 to 21 of SEQ ID NO:112 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 22. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the km225\_1 protein.

30

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone km225\_1 should be approximately 2300 bp.

The nucleotide sequence disclosed herein for km225\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. km225\_1 demonstrated at least some similarity with sequences identified as AA101603 (zk94h09.s1 Soares pregnant uterus NbHPU Homo sapiens cDNA clone 490529 3' similar to contains Alu repetitive element; mRNA sequence). Based upon sequence similarity, km225\_1 proteins and each similar protein or peptide may share at least some activity.

#### Clone "mj301\_1"

A polynucleotide of the present invention has been identified as clone "mj301\_1". mj301\_1 was isolated from a human adult lymph node cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. mj301\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "mj301\_1 protein").

The nucleotide sequence of mj301\_1 as presently determined is reported in SEQ ID NO:113, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the mj301\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:114. Amino acids 65 to 77 of SEQ ID NO:114 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 78. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the mj301\_1 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone mj301\_1 should be approximately 2760 bp; however, a band of 550 bp has been detected in restriction digests, possibly due to an internal EcoRI or NotI restriction site in the clone.

The nucleotide sequence disclosed herein for mj301\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. mj301\_1 demonstrated at least some similarity with sequences identified as AA053085 (zl73d01.s1 Stratagene colon (#937204) Homo sapiens cDNA

clone 510241 3'), AA347293 (EST53566 Fetal heart II Homo sapiens cDNA 5' end), AA813287 (ai76a07.s1 Soares testis NHT Homo sapiens cDNA clone 1376724 3', mRNA sequence), R45713 (Ha117-f Homo sapiens cDNA clone a117-f), T20114 (Human gene signature HUMGS01258), U46278 (Human clone xs252 mRNA sequence), Z36823 (H.sapiens (xs170) mRNA), and Z36832 (H.sapiens (xs170) mRNA). The human xs170 sequence is differentially expressed in pancreatic cancer cells. The predicted amino acid sequence disclosed herein for mj301\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted mj301\_1 protein demonstrated at least some similarity to the sequence identified as U07818 (putative phospho-beta-glucosidase [Bacillus stearothermophilus]). Based upon sequence similarity, mj301\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts an additional potential transmembrane domain within the mj301\_1 protein sequence centered around amino acid 60 of SEQ ID NO:114.

#### Clone "ml10\_7"

A polynucleotide of the present invention has been identified as clone "ml10\_7". ml10\_7 was isolated from a human adult brain (caudate nucleus) cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. ml10\_7 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "ml10\_7 protein").

The nucleotide sequence of ml10\_7 as presently determined is reported in SEQ ID NO:115, and includes a poly(A) tail. What applicants presently believe to be the proper reading frame and the predicted amino acid sequence of the ml10\_7 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:116. Amino acids 30 to 42 of SEQ ID NO:116 are a predicted leader/signal sequence, with the predicted mature amino acid sequence beginning at amino acid 43. Due to the hydrophobic nature of the predicted leader/signal sequence, it is likely to act as a transmembrane domain should the predicted leader/signal sequence not be separated from the remainder of the ml10\_7 protein.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone ml10\_7 should be approximately 1600 bp.

The nucleotide sequence disclosed herein for ml10\_7 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. ml10\_7 demonstrated at least some similarity with sequences identified as AA411457 (zv30f06.s1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 3'), AA411585 (zv30f06.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 755171 5', mRNA sequence), AA485512 (zx90b02.r1 Soares ovary tumor NbHOT Homo sapiens cDNA clone 810987 5'), R97588 (yq59b05.r1 Homo sapiens cDNA clone 200049 5' similar to contains MSR1 repetitive element), and T23020 (Human gene signature HUMGS04748). The predicted amino acid sequence disclosed herein for ml10\_7 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted ml10\_7 protein demonstrated at least some similarity to the sequence identified as R56978 (Human myotonic dystrophy gene protein). Based upon sequence similarity, ml10\_7 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts four additional potential transmembrane domains within the ml10\_7 protein sequence, centered approximately around amino acids 20, 55 (between residues 50 and 60), 85 (between residues 80 and 89), and 175 (between residues 169 and 180) of SEQ ID NO:116, respectively. ml10\_7 appears to represent one member of a group of multiple alternatively spliced transcripts.

#### Clone "my340\_1"

A polynucleotide of the present invention has been identified as clone "my340\_1". my340\_1 was isolated from a human fetal brain cDNA library using methods which are selective for cDNAs encoding secreted proteins (see U.S. Pat. No. 5,536,637), or was identified as encoding a secreted or transmembrane protein on the basis of computer analysis of the amino acid sequence of the encoded protein. my340\_1 is a full-length clone, including the entire coding sequence of a secreted protein (also referred to herein as "my340\_1 protein").

The nucleotide sequence of my340\_1 as presently determined is reported in SEQ ID NO:117, and includes a poly(A) tail. What applicants presently believe to be the proper

reading frame and the predicted amino acid sequence of the my340\_1 protein corresponding to the foregoing nucleotide sequence is reported in SEQ ID NO:118.

The EcoRI/NotI restriction fragment obtainable from the deposit containing clone my340\_1 should be approximately 1800 bp.

5        The nucleotide sequence disclosed herein for my340\_1 was searched against the GenBank and GeneSeq nucleotide sequence databases using BLASTN/BLASTX and FASTA search protocols. my340\_1 demonstrated at least some similarity with sequences identified as AA469015 (nc79g10.r1 NCI\_CGAP\_Pr2 Homo sapiens cDNA clone IMAGE:783618), H85290 (yv86f01.r1 Homo sapiens cDNA clone 249625 5'), L29074  
10 (Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds), M86699 (Human kinase (TTK) mRNA, complete cds), W19755 (zb38f08.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 305895 5'), W63667 (zc57h10.r1 Soares parathyroid tumor NbHPA Homo sapiens cDNA clone 326467 5', mRNA sequence), and Z84478 (Human DNA sequence). The predicted amino  
15 acid sequence disclosed herein for my340\_1 was searched against the GenPept and GeneSeq amino acid sequence databases using the BLASTX search protocol. The predicted my340\_1 protein demonstrated at least some similarity to the sequence identified as M86699 (kinase [Homo sapiens]). The human TTK kinase can phosphorylate serine, threonine, and tyrosine hydroxyamino acids. Based upon sequence similarity,  
20 my340\_1 proteins and each similar protein or peptide may share at least some activity. The TopPredII computer program predicts a potential transmembrane domain within the my340\_1 protein sequence centered around amino acid 50 of SEQ ID NO:28.

#### Deposit of Clones

25        Clones bn365\_53, bo342\_2, dn721\_8, dn834\_1, pd278\_5, pe80\_1, pm113\_1, pm749\_8, pt31\_4, and pv296\_5 were deposited on May 7, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98752, from which each clone comprising a particular polynucleotide is obtainable.

30        Clones er311\_20, fh149\_12, pc201\_6, pl87\_1, and pm514\_4 were deposited on June 2, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty



and were given the accession number ATCC 98781, from which each clone comprising a particular polynucleotide is obtainable.

Clones co155\_12, fn189\_13, lv2\_47, ml243\_1, pm96\_9, pu261\_1, pw214\_15, qb56\_19, qc646\_1, qf116\_2, and qf662\_3 were deposited on July 2, 1998 with the American  
5 Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98808, from which each clone comprising a particular polynucleotide is obtainable.

Clones am748\_5, cj507\_1, cn922\_5, cw691\_11, cw1000\_2, cw1640\_1, d24\_1,  
10 dd426\_1, and di393\_2 were deposited on July 16, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98817, from which each clone comprising a particular polynucleotide is obtainable.

Clones dj167\_2, dw665\_4, dx146\_12, dx219\_13, fm3\_1, h225\_1, kj320\_1, ml236\_5,  
15 and pu282\_10, were deposited on July 16, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98818, from which each clone comprising a particular polynucleotide is obtainable.

Clones at94\_2, bf169\_13, bl152\_12, bz578\_1, cb123\_1, ch245\_1, cj378\_3, cw1481\_1,  
20 dd119\_4, df202\_3, km225\_1, mj301\_1, ml10\_7, and my340\_1 were deposited on July 22, 1998 with the American Type Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and were given the accession number ATCC 98822, from which each clone comprising a particular polynucleotide is obtainable.

Clone dj167\_19 was deposited on February 5, 1999 with the American Type  
25 Culture Collection (10801 University Boulevard, Manassas, Virginia 20110-2209 U.S.A.) as an original deposit under the Budapest Treaty and was given the accession number ATCC 207090, from which the dj167\_19 clone comprising a particular polynucleotide is obtainable.

30 All restrictions on the availability to the public of the deposited material will be irrevocably removed upon the granting of the patent, except for the requirements specified in 37 C.F.R. § 1.808(b), and the term of the deposit will comply with 37 C.F.R. § 1.806.

Each clone has been transfected into separate bacterial cells (*E. coli*) in the composite deposits above. Each clone can be removed from the vector in which it was deposited by performing an EcoRI/NotI digestion (5' site, EcoRI; 3' site, NotI) to produce the appropriate fragment for such clone. Each clone was deposited in either the pED6 or pNOTs vector depicted in Figures 1A and 1B, respectively. The pED6dpc2 vector ("pED6") was derived from pED6dpc1 by insertion of a new polylinker to facilitate cDNA cloning (Kaufman *et al.*, 1991, *Nucleic Acids Res.* **19**: 4485-4490); the pNOTs vector was derived from pMT2 (Kaufman *et al.*, 1989, *Mol. Cell. Biol.* **9**: 946-958) by deletion of the DHFR sequences, insertion of a new polylinker, and insertion of the M13 origin of replication in the ClaI site. In some instances, the deposited clone can become "flipped" (i.e., in the reverse orientation) in the deposited isolate. In such instances, the cDNA insert can still be isolated by digestion with EcoRI and NotI. However, NotI will then produce the 5' site and EcoRI will produce the 3' site for placement of the cDNA in proper orientation for expression in a suitable vector. The cDNA may also be expressed from the vectors in which they were deposited.

Bacterial cells containing a particular clone can be obtained from the composite deposit as follows:

An oligonucleotide probe or probes should be designed to the sequence that is known for that particular clone. This sequence can be derived from the sequences provided herein, or from a combination of those sequences. The sequence of an oligonucleotide probe that was used to isolate or to sequence each full-length clone is identified below, and should be most reliable in isolating the clone of interest.

	<u>Clone</u>	<u>Probe Sequence</u>
25	bn365_53	SEQ ID NO:119
	bo342_2	SEQ ID NO:120
	dn721_8	SEQ ID NO:121
	dn834_1	SEQ ID NO:122
	pd278_5	SEQ ID NO:123
30	pe80_1	SEQ ID NO:124
	pm113_1	SEQ ID NO:125
	pm749_8	SEQ ID NO:126
	pt31_4	SEQ ID NO:127
	pv296_5	SEQ ID NO:128

	er311_20	SEQ ID NO:129
	fh149_12	SEQ ID NO:130
	pc201_6	SEQ ID NO:131
	pl87_1	SEQ ID NO:132
5	pm514_4	SEQ ID NO:133
	co155_12	SEQ ID NO:134
	fn189_13	SEQ ID NO:135
	lv2_47	SEQ ID NO:136
	ml243_1	SEQ ID NO:137
10	pm96_9	SEQ ID NO:138
	pu261_1	SEQ ID NO:139
	pw214_15	SEQ ID NO:140
	qb56_19	SEQ ID NO:141
	qc646_1	SEQ ID NO:142
15	qf116_2	SEQ ID NO:143
	qf662_3	SEQ ID NO:144
	am748_5	SEQ ID NO:145
	cj507_1	SEQ ID NO:146
	cn922_5	SEQ ID NO:147
20	cw691_11	SEQ ID NO:148
	cw1000_2	SEQ ID NO:149
	cw1640_1	SEQ ID NO:150
	d24_1	SEQ ID NO:151
	dd426_1	SEQ ID NO:152
25	di393_2	SEQ ID NO:153
	dj167_2	SEQ ID NO:154
	dw665_4	SEQ ID NO:155
	dx146_12	SEQ ID NO:156
	dx219_13	SEQ ID NO:157
30	fm3_1	SEQ ID NO:158
	h225_1	SEQ ID NO:159
	kj320_1	SEQ ID NO:160
	ml236_5	SEQ ID NO:161
	pu282_10	SEQ ID NO:162

	at94_2	SEQ ID NO:163
	bf169_13	SEQ ID NO:164
	bl152_12	SEQ ID NO:165
	bz578_1	SEQ ID NO:166
5	cb123_1	SEQ ID NO:167
	ch245_1	SEQ ID NO:168
	cj378_3	SEQ ID NO:169
	cw1481_1	SEQ ID NO:170
	dd119_4	SEQ ID NO:171
10	df202_3	SEQ ID NO:172
	km225_1	SEQ ID NO:173
	mj301_1	SEQ ID NO:174
	ml10_7	SEQ ID NO:175
	my340_1	SEQ ID NO:176

15

In the sequences listed above which include an N at position 2, that position is occupied in preferred probes/primers by a biotinylated phosphoramidite residue rather than a nucleotide (such as, for example, that produced by use of biotin phosphoramidite (1-dimethoxytrityloxy-2-(N-biotinyl-4-aminobutyl)-propyl-3-O-(2-cyanoethyl)-(N,N-diisopropyl)-phosphoramidite) (Glen Research, cat. no. 10-1953)).

20

The design of the oligonucleotide probe should preferably follow these parameters:

- (a) It should be designed to an area of the sequence which has the fewest ambiguous bases ("N's"), if any;
- 25 (b) It should be designed to have a  $T_m$  of approx. 80 ° C (assuming 2° for each A or T and 4 degrees for each G or C).

The oligonucleotide should preferably be labeled with  $\gamma$ -<sup>32</sup>P ATP (specific activity 6000 Ci/mmol) and T4 polynucleotide kinase using commonly employed techniques for labeling oligonucleotides. Other labeling techniques can also be used. Unincorporated label should preferably be removed by gel filtration chromatography or other established methods. The amount of radioactivity incorporated into the probe should be quantitated by measurement in a scintillation counter. Preferably, specific activity of the resulting probe should be approximately 4e+6 dpm/pmol.

30

5 The bacterial culture containing the pool of full-length clones should preferably be thawed and 100  $\mu$ l of the stock used to inoculate a sterile culture flask containing 25 ml of sterile L-broth containing ampicillin at 100  $\mu$ g/ml. The culture should preferably be grown to saturation at 37°C, and the saturated culture should preferably be diluted in fresh L-broth. Aliquots of these dilutions should preferably be plated to determine the dilution and volume which will yield approximately 5000 distinct and well-separated colonies on solid bacteriological media containing L-broth containing ampicillin at 100  $\mu$ g/ml and agar at 1.5% in a 150 mm petri dish when grown overnight at 37°C. Other known methods of obtaining distinct, well-separated colonies can also be employed.

10 Standard colony hybridization procedures should then be used to transfer the colonies to nitrocellulose filters and lyse, denature and bake them.

The filter is then preferably incubated at 65°C for 1 hour with gentle agitation in 6X SSC (20X stock is 175.3 g NaCl/liter, 88.2 g Na citrate/liter, adjusted to pH 7.0 with NaOH) containing 0.5% SDS, 100  $\mu$ g/ml of yeast RNA, and 10 mM EDTA (approximately 15 10 mL per 150 mm filter). Preferably, the probe is then added to the hybridization mix at a concentration greater than or equal to 1e+6 dpm/mL. The filter is then preferably incubated at 65°C with gentle agitation overnight. The filter is then preferably washed in 500 mL of 2X SSC/0.5% SDS at room temperature without agitation, preferably followed by 500 mL of 2X SSC/0.1% SDS at room temperature with gentle shaking for 15 minutes. 20 A third wash with 0.1X SSC/0.5% SDS at 65°C for 30 minutes to 1 hour is optional. The filter is then preferably dried and subjected to autoradiography for sufficient time to visualize the positives on the X-ray film. Other known hybridization methods can also be employed.

The positive colonies are picked, grown in culture, and plasmid DNA isolated 25 using standard procedures. The clones can then be verified by restriction analysis, hybridization analysis, or DNA sequencing.

Fragments of the proteins of the present invention which are capable of exhibiting biological activity are also encompassed by the present invention. Fragments of the protein may be in linear form or they may be cyclized using known methods, for example, 30 as described in H.U. Saragovi, *et al.*, Bio/Technology 10, 773-778 (1992) and in R.S. McDowell, *et al.*, J. Amer. Chem. Soc. 114, 9245-9253 (1992), both of which are incorporated herein by reference. Such fragments may be fused to carrier molecules such as immunoglobulins for many purposes, including increasing the valency of protein binding sites. For example, fragments of the protein may be fused through "linker" sequences to

the Fc portion of an immunoglobulin. For a bivalent form of the protein, such a fusion could be to the Fc portion of an IgG molecule. Other immunoglobulin isotypes may also be used to generate such fusions. For example, a protein - IgM fusion would generate a decavalent form of the protein of the invention.

5           The present invention also provides both full-length and mature forms of the disclosed proteins. The full-length form of the such proteins is identified in the sequence listing by translation of the nucleotide sequence of each disclosed clone. The mature form(s) of such protein may be obtained by expression of the disclosed full-length polynucleotide (preferably those deposited with ATCC) in a suitable mammalian cell or  
10 other host cell. The sequence(s) of the mature form(s) of the protein may also be determinable from the amino acid sequence of the full-length form.

          The present invention also provides genes corresponding to the polynucleotide sequences disclosed herein. "Corresponding genes" are the regions of the genome that are transcribed to produce the mRNAs from which cDNA polynucleotide sequences are  
15 derived and may include contiguous regions of the genome necessary for the regulated expression of such genes. Corresponding genes may therefore include but are not limited to coding sequences, 5' and 3' untranslated regions, alternatively spliced exons, introns, promoters, enhancers, and silencer or suppressor elements. The corresponding genes can be isolated in accordance with known methods using the sequence information disclosed  
20 herein. Such methods include the preparation of probes or primers from the disclosed sequence information for identification and/or amplification of genes in appropriate genomic libraries or other sources of genomic materials. An "isolated gene" is a gene that has been separated from the adjacent coding sequences, if any, present in the genome of the organism from which the gene was isolated.

25           The chromosomal location corresponding to the polynucleotide sequences disclosed herein may also be determined, for example by hybridizing appropriately labeled polynucleotides of the present invention to chromosomes *in situ*. It may also be possible to determine the corresponding chromosomal location for a disclosed polynucleotide by identifying significantly similar nucleotide sequences in public  
30 databases, such as expressed sequence tags (ESTs), that have already been mapped to particular chromosomal locations. For at least some of the polynucleotide sequences disclosed herein, public database sequences having at least some similarity to the polynucleotide of the present invention have been listed by database accession number. Searches using the GenBank accession numbers of these public database sequences can

then be performed at an Internet site provided by the National Center for Biotechnology Information having the address <http://www.ncbi.nlm.nih.gov/UniGene/>, in order to identify "UniGene clusters" of overlapping sequences. Many of the "UniGene clusters" so identified will already have been mapped to particular chromosomal sites.

- 5           Organisms that have enhanced, reduced, or modified expression of the gene(s) corresponding to the polynucleotide sequences disclosed herein are provided. The desired change in gene expression can be achieved through the use of antisense polynucleotides or ribozymes that bind and/or cleave the mRNA transcribed from the gene (Albert and Morris, 1994, *Trends Pharmacol. Sci.* **15**(7): 250-254; Lavarosky *et al.*, 1997, *Biochem. Mol. Med.* **62**(1): 11-22; and Hampel, 1998, *Prog. Nucleic Acid Res. Mol. Biol.* **58**: 1-39; all of which are incorporated by reference herein). Transgenic animals that have multiple copies of the gene(s) corresponding to the polynucleotide sequences disclosed herein, preferably produced by transformation of cells with genetic constructs that are stably maintained within the transformed cells and their progeny, are provided.
- 10           Transgenic animals that have modified genetic control regions that increase or reduce gene expression levels, or that change temporal or spatial patterns of gene expression, are also provided (see European Patent No. 0 649 464 B1, incorporated by reference herein). In addition, organisms are provided in which the gene(s) corresponding to the polynucleotide sequences disclosed herein have been partially or completely inactivated,
- 15           through insertion of extraneous sequences into the corresponding gene(s) or through deletion of all or part of the corresponding gene(s). Partial or complete gene inactivation can be accomplished through insertion, preferably followed by imprecise excision, of transposable elements (Plasterk, 1992, *Bioessays* **14**(9): 629-633; Zwaal *et al.*, 1993, *Proc. Natl. Acad. Sci. USA* **90**(16): 7431-7435; Clark *et al.*, 1994, *Proc. Natl. Acad. Sci. USA* **91**(2): 719-722;
- 20           all of which are incorporated by reference herein), or through homologous recombination, preferably detected by positive/negative genetic selection strategies (Mansour *et al.*, 1988, *Nature* **336**: 348-352; U.S. Patent Nos. 5,464,764; 5,487,992; 5,627,059; 5,631,153; 5,614,396; 5,616,491; and 5,679,523; all of which are incorporated by reference herein). These organisms with altered gene expression are preferably eukaryotes and more preferably
- 25           are mammals. Such organisms are useful for the development of non-human models for the study of disorders involving the corresponding gene(s), and for the development of assay systems for the identification of molecules that interact with the protein product(s) of the corresponding gene(s).
- 30

Where the protein of the present invention is membrane-bound (e.g., is a receptor), the present invention also provides for soluble forms of such protein. In such forms, part or all of the intracellular and transmembrane domains of the protein are deleted such that the protein is fully secreted from the cell in which it is expressed. The intracellular and transmembrane domains of proteins of the invention can be identified in accordance with known techniques for determination of such domains from sequence information. For example, the TopPredII computer program can be used to predict the location of transmembrane domains in an amino acid sequence, domains which are described by the location of the center of the transmembrane domain, with at least ten transmembrane amino acids on each side of the reported central residue(s).

Proteins and protein fragments of the present invention include proteins with amino acid sequence lengths that are at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of a disclosed protein and have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with that disclosed protein, where sequence identity is determined by comparing the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Also included in the present invention are proteins and protein fragments that contain a segment preferably comprising 8 or more (more preferably 20 or more, most preferably 30 or more) contiguous amino acids that shares at least 75% sequence identity (more preferably, at least 85% identity; most preferably at least 95% identity) with any such segment of any of the disclosed proteins.

In particular, sequence identity may be determined using WU-BLAST (Washington University BLAST) version 2.0 software, which builds upon WU-BLAST version 1.4, which in turn is based on the public domain NCBI-BLAST version 1.4 (Altschul and Gish, 1996, Local alignment statistics, Doolittle *ed.*, *Methods in Enzymology* **266**: 460-480; Altschul *et al.*, 1990, Basic local alignment search tool, *Journal of Molecular Biology* **215**: 403-410; Gish and States, 1993, Identification of protein coding regions by database similarity search, *Nature Genetics* **3**: 266-272; Karlin and Altschul, 1993, Applications and statistics for multiple high-scoring segments in molecular sequences, *Proc. Natl. Acad. Sci. USA* **90**: 5873-5877; all of which are incorporated by reference herein). WU-BLAST version 2.0 executable programs for several UNIX platforms can be downloaded from <ftp://blast.wustl.edu/blast/executables>. The complete suite of search programs (BLASTP, BLASTN, BLASTX, TBLASTN, and TBLASTX) is



provided at that site, in addition to several support programs. WU-BLAST 2.0 is copyrighted and may not be sold or redistributed in any form or manner without the express written consent of the author; but the posted executables may otherwise be freely used for commercial, nonprofit, or academic purposes. In all search programs in the suite

5 -- BLASTP, BLASTN, BLASTX, TBLASTN and TBLASTX -- the gapped alignment routines are integral to the database search itself, and thus yield much better sensitivity and selectivity while producing the more easily interpreted output. Gapping can optionally be turned off in all of these programs, if desired. The default penalty (Q) for a gap of length one is Q=9 for proteins and BLASTP, and Q=10 for BLASTN, but may be changed to any

10 integer value including zero, one through eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one through one hundred, etc. The default per-residue penalty for extending a gap (R) is R=2 for proteins and BLASTP, and R=10 for BLASTN, but may be changed to any integer value including zero, one, two, three, four, five, six, seven, eight, nine, ten, eleven, twelve through twenty, twenty-one through fifty, fifty-one

15 through one hundred, etc. Any combination of values for Q and R can be used in order to align sequences so as to maximize overlap and identity while minimizing sequence gaps. The default amino acid comparison matrix is BLOSUM62, but other amino acid comparison matrices such as PAM can be utilized.

Species homologues of the disclosed polynucleotides and proteins are also

20 provided by the present invention. As used herein, a "species homologue" is a protein or polynucleotide with a different species of origin from that of a given protein or polynucleotide, but with significant sequence similarity to the given protein or polynucleotide. Preferably, polynucleotide species homologues have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with

25 the given polynucleotide, and protein species homologues have at least 30% sequence identity (more preferably, at least 45% identity; most preferably at least 60% identity) with the given protein, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides or the amino acid sequences of the proteins when aligned so as to maximize overlap and identity while minimizing sequence gaps. Species

30 homologues may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from the desired species. Preferably, species homologues are those isolated from mammalian

species. Most preferably, species homologues are those isolated from certain mammalian species such as, for example, *Pan troglodytes*, *Gorilla gorilla*, *Pongo pygmaeus*, *Hylobates concolor*, *Macaca mulatta*, *Papio papio*, *Papio hamadryas*, *Cercopithecus aethiops*, *Cebus capucinus*, *Aotus trivirgatus*, *Sanguinus oedipus*, *Microcebus murinus*, *Mus musculus*, *Rattus norvegicus*,  
5 *Cricetulus griseus*, *Felis catus*, *Mustela vison*, *Canis familiaris*, *Oryctolagus cuniculus*, *Bos taurus*, *Ovis aries*, *Sus scrofa*, and *Equus caballus*, for which genetic maps have been created allowing the identification of syntenic relationships between the genomic organization of genes in one species and the genomic organization of the related genes in another species (O'Brien and Seuáñez, 1988, *Ann. Rev. Genet.* **22**: 323-351; O'Brien *et al.*, 1993, *Nature*  
10 *Genetics* **3**:103-112; Johansson *et al.*, 1995, *Genomics* **25**: 682-690; Lyons *et al.*, 1997, *Nature Genetics* **15**: 47-56; O'Brien *et al.*, 1997, *Trends in Genetics* **13**(10): 393-399; Carver and Stubbs, 1997, *Genome Research* **7**:1123-1137; all of which are incorporated by reference herein).

The invention also encompasses allelic variants of the disclosed polynucleotides or proteins; that is, naturally-occurring alternative forms of the isolated polynucleotides  
15 which also encode proteins which are identical or have significantly similar sequences to those encoded by the disclosed polynucleotides. Preferably, allelic variants have at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% identity) with the given polynucleotide, where sequence identity is determined by comparing the nucleotide sequences of the polynucleotides when aligned so as to maximize  
20 overlap and identity while minimizing sequence gaps. Allelic variants may be isolated and identified by making suitable probes or primers from the sequences provided herein and screening a suitable nucleic acid source from individuals of the appropriate species.

The invention also includes polynucleotides with sequences complementary to those of the polynucleotides disclosed herein.

25 The present invention also includes polynucleotides that hybridize under reduced stringency conditions, more preferably stringent conditions, and most preferably highly stringent conditions, to polynucleotides described herein. Examples of stringency conditions are shown in the table below: highly stringent conditions are those that are at least as stringent as, for example, conditions A-F; stringent conditions are at least as  
30 stringent as, for example, conditions G-L; and reduced stringency conditions are at least as stringent as, for example, conditions M-R.

Stringency Condition	Polynucleotide Hybrid	Hybrid Length (bp) <sup>‡</sup>	Hybridization Temperature and Buffer <sup>†</sup>	Wash Temperature and Buffer <sup>†</sup>
5	A	≥ 50	65°C; 1xSSC -or- 42°C; 1xSSC, 50% formamide	65°C; 0.3xSSC
	B	<50	T <sub>B</sub> <sup>*</sup> ; 1xSSC	T <sub>B</sub> <sup>*</sup> ; 1xSSC
	C	≥ 50	67°C; 1xSSC -or- 45°C; 1xSSC, 50% formamide	67°C; 0.3xSSC
	D	<50	T <sub>D</sub> <sup>*</sup> ; 1xSSC	T <sub>D</sub> <sup>*</sup> ; 1xSSC
	E	≥ 50	70°C; 1xSSC -or- 50°C; 1xSSC, 50% formamide	70°C; 0.3xSSC
	F	<50	T <sub>F</sub> <sup>*</sup> ; 1xSSC	T <sub>F</sub> <sup>*</sup> ; 1xSSC
10	G	≥ 50	65°C; 4xSSC -or- 42°C; 4xSSC, 50% formamide	65°C; 1xSSC
	H	<50	T <sub>H</sub> <sup>*</sup> ; 4xSSC	T <sub>H</sub> <sup>*</sup> ; 4xSSC
	I	≥ 50	67°C; 4xSSC -or- 45°C; 4xSSC, 50% formamide	67°C; 1xSSC
	J	<50	T <sub>J</sub> <sup>*</sup> ; 4xSSC	T <sub>J</sub> <sup>*</sup> ; 4xSSC
	K	≥ 50	70°C; 4xSSC -or- 50°C; 4xSSC, 50% formamide	67°C; 1xSSC
	L	<50	T <sub>L</sub> <sup>*</sup> ; 2xSSC	T <sub>L</sub> <sup>*</sup> ; 2xSSC
15	M	≥ 50	50°C; 4xSSC -or- 40°C; 6xSSC, 50% formamide	50°C; 2xSSC
	N	<50	T <sub>N</sub> <sup>*</sup> ; 6xSSC	T <sub>N</sub> <sup>*</sup> ; 6xSSC
	O	≥ 50	55°C; 4xSSC -or- 42°C; 6xSSC, 50% formamide	55°C; 2xSSC
	P	<50	T <sub>P</sub> <sup>*</sup> ; 6xSSC	T <sub>P</sub> <sup>*</sup> ; 6xSSC
	Q	≥ 50	60°C; 4xSSC -or- 45°C; 6xSSC, 50% formamide	60°C; 2xSSC
	R	<50	T <sub>R</sub> <sup>*</sup> ; 4xSSC	T <sub>R</sub> <sup>*</sup> ; 4xSSC

<sup>‡</sup>: The hybrid length is that anticipated for the hybridized region(s) of the hybridizing polynucleotides. When hybridizing a polynucleotide to a target polynucleotide of unknown sequence, the hybrid length is assumed to be that of the hybridizing polynucleotide. When polynucleotides of known sequence are hybridized, the hybrid length can be determined by aligning the sequences of the polynucleotides and identifying the region or regions of optimal sequence complementarity.

<sup>†</sup>: SSPE (1xSSPE is 0.15M NaCl, 10mM NaH<sub>2</sub>PO<sub>4</sub>, and 1.25mM EDTA, pH 7.4) can be substituted for SSC (1xSSC is 0.15M NaCl and 15mM sodium citrate) in the hybridization and wash buffers; washes are performed for 15 minutes after hybridization is complete.

<sup>\*</sup>T<sub>B</sub> - T<sub>R</sub>: The hybridization temperature for hybrids anticipated to be less than 50 base pairs in length should be 5-10°C less than the melting temperature (T<sub>m</sub>) of the hybrid, where T<sub>m</sub> is determined according to the following equations. For hybrids less than 18 base pairs in length, T<sub>m</sub>(°C) = 2(# of A + T bases) + 4(# of G + C bases). For hybrids between 18 and 49 base pairs in length, T<sub>m</sub>(°C) = 81.5 + 16.6(log<sub>10</sub>[Na<sup>+</sup>]) + 0.41(%G+C) - (600/N), where N is the number of bases in the hybrid, and [Na<sup>+</sup>] is the concentration of sodium ions in the hybridization buffer ([Na<sup>+</sup>] for 1xSSC = 0.165 M).

Additional examples of stringency conditions for polynucleotide hybridization are provided in Sambrook, J., E.F. Fritsch, and T. Maniatis, 1989, *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, chapters 9 and 11, and *Current Protocols in Molecular Biology*, 1995, F.M. Ausubel et al., eds., John Wiley & Sons, Inc., sections 2.10 and 6.3-6.4, incorporated herein by reference.

Preferably, each such hybridizing polynucleotide has a length that is at least 25% (more preferably at least 50%, and most preferably at least 75%) of the length of the polynucleotide of the present invention to which it hybridizes, and has at least 60% sequence identity (more preferably, at least 75% identity; most preferably at least 90% or 95% identity) with the polynucleotide of the present invention to which it hybridizes, where sequence identity is determined by comparing the sequences of the hybridizing polynucleotides when aligned so as to maximize overlap and identity while minimizing sequence gaps.

The isolated polynucleotide of the invention may be operably linked to an expression control sequence such as the pMT2 or pED expression vectors disclosed in Kaufman *et al.*, *Nucleic Acids Res.* 19, 4485-4490 (1991), in order to produce the protein recombinantly. Many suitable expression control sequences are known in the art. General methods of expressing recombinant proteins are also known and are exemplified in R. Kaufman, *Methods in Enzymology* 185, 537-566 (1990). As defined herein "operably linked" means that the isolated polynucleotide of the invention and an expression control sequence are situated within a vector or cell in such a way that the protein is expressed by a host cell which has been transformed (transfected) with the ligated polynucleotide/expression control sequence.

A number of types of cells may act as suitable host cells for expression of the protein. Mammalian host cells include, for example, monkey COS cells, Chinese Hamster Ovary (CHO) cells, human kidney 293 cells, human epidermal A431 cells, human Colo205 cells, 3T3 cells, CV-1 cells, other transformed primate cell lines, normal diploid cells, cell strains derived from *in vitro* culture of primary tissue, primary explants, HeLa cells, mouse L cells, BHK, HL-60, U937, HaK or Jurkat cells.

Alternatively, it may be possible to produce the protein in lower eukaryotes such as yeast or in prokaryotes such as bacteria. Potentially suitable yeast strains include *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Kluyveromyces* strains, *Candida*, or any yeast strain capable of expressing heterologous proteins. Potentially suitable bacterial strains include *Escherichia coli*, *Bacillus subtilis*, *Salmonella typhimurium*, or any bacterial

strain capable of expressing heterologous proteins. If the protein is made in yeast or bacteria, it may be necessary to modify the protein produced therein, for example by phosphorylation or glycosylation of the appropriate sites, in order to obtain the functional protein. Such covalent attachments may be accomplished using known chemical or enzymatic methods.

The protein may also be produced by operably linking the isolated polynucleotide of the invention to suitable control sequences in one or more insect expression vectors, and employing an insect expression system. Materials and methods for baculovirus/insect cell expression systems are commercially available in kit form from, *e.g.*, Invitrogen, San Diego, California, U.S.A. (the MaxBac® kit), and such methods are well known in the art, as described in Summers and Smith, Texas Agricultural Experiment Station Bulletin No. 1555 (1987), incorporated herein by reference. As used herein, an insect cell capable of expressing a polynucleotide of the present invention is "transformed."

The protein of the invention may be prepared by culturing transformed host cells under culture conditions suitable to express the recombinant protein. The resulting expressed protein may then be purified from such culture (*i.e.*, from culture medium or cell extracts) using known purification processes, such as gel filtration and ion exchange chromatography. The purification of the protein may also include an affinity column containing agents which will bind to the protein; one or more column steps over such affinity resins as concanavalin A-agarose, heparin-toyopearl® or Cibacrom blue 3GA Sepharose®; one or more steps involving hydrophobic interaction chromatography using such resins as phenyl ether, butyl ether, or propyl ether; or immunoaffinity chromatography.

Alternatively, the protein of the invention may also be expressed in a form which will facilitate purification. For example, it may be expressed as a fusion protein, such as those of maltose binding protein (MBP), glutathione-S-transferase (GST) or thioredoxin (TRX). Kits for expression and purification of such fusion proteins are commercially available from New England BioLabs (Beverly, MA), Pharmacia (Piscataway, NJ) and Invitrogen Corporation (Carlsbad, CA), respectively. The protein can also be tagged with an epitope and subsequently purified by using a specific antibody directed to such epitope. One such epitope ("Flag") is commercially available from the Eastman Kodak Company (New Haven, CT).

Finally, one or more reverse-phase high performance liquid chromatography (RP-HPLC) steps employing hydrophobic RP-HPLC media, e.g., silica gel having pendant methyl or other aliphatic groups, can be employed to further purify the protein. Some or all of the foregoing purification steps, in various combinations, can also be employed to provide a substantially homogeneous isolated recombinant protein. The protein thus purified is substantially free of other mammalian proteins and is defined in accordance with the present invention as an "isolated protein."

The protein of the invention may also be expressed as a product of transgenic animals, e.g., as a component of the milk of transgenic cows, goats, pigs, or sheep which are characterized by somatic or germ cells containing a nucleotide sequence encoding the protein.

The protein may also be produced by known conventional chemical synthesis. Methods for constructing the proteins of the present invention by synthetic means are known to those skilled in the art. The synthetically-constructed protein sequences, by virtue of sharing primary, secondary or tertiary structural and/or conformational characteristics with proteins may possess biological properties in common therewith, including protein activity. Thus, they may be employed as biologically active or immunological substitutes for natural, purified proteins in screening of therapeutic compounds and in immunological processes for the development of antibodies.

The proteins provided herein also include proteins characterized by amino acid sequences similar to those of purified proteins but into which modification are naturally provided or deliberately engineered. For example, modifications in the peptide or DNA sequences can be made by those skilled in the art using known techniques. Modifications of interest in the protein sequences may include the alteration, substitution, replacement, insertion or deletion of a selected amino acid residue in the coding sequence. For example, one or more of the cysteine residues may be deleted or replaced with another amino acid to alter the conformation of the molecule. Techniques for such alteration, substitution, replacement, insertion or deletion are well known to those skilled in the art (see, e.g., U.S. Patent No. 4,518,584). Preferably, such alteration, substitution, replacement, insertion or deletion retains the desired activity of the protein.

Other fragments and derivatives of the sequences of proteins which would be expected to retain protein activity in whole or in part and may thus be useful for screening or other immunological methodologies may also be easily made by those skilled in the art

given the disclosures herein. Such modifications are believed to be encompassed by the present invention.

## USES AND BIOLOGICAL ACTIVITY

5           The polynucleotides and proteins of the present invention are expected to exhibit one or more of the uses or biological activities (including those associated with assays cited herein) identified below. Uses or activities described for proteins of the present invention may be provided by administration or use of such proteins or by administration or use of polynucleotides encoding such proteins (such as, for example, in gene therapies  
10 or vectors suitable for introduction of DNA).

### Research Uses and Utilities

          The polynucleotides provided by the present invention can be used by the research community for various purposes. The polynucleotides can be used to express  
15 recombinant protein for analysis, characterization or therapeutic use; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in disease states); as molecular weight markers on Southern gels; as chromosome markers or tags (when labeled) to identify chromosomes or to map related gene positions; to compare  
20 with endogenous DNA sequences in patients to identify potential genetic disorders; as probes to hybridize and thus discover novel, related DNA sequences; as a source of information to derive PCR primers for genetic fingerprinting; as a probe to "subtract-out" known sequences in the process of discovering other novel polynucleotides; for selecting and making oligomers for attachment to a "gene chip" or other support, including for  
25 examination of expression patterns; to raise anti-protein antibodies using DNA immunization techniques; and as an antigen to raise anti-DNA antibodies or elicit another immune response. Where the polynucleotide encodes a protein which binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the polynucleotide can also be used in interaction trap assays (such as, for example, those  
30 described in Gyuris *et al.*, 1993, *Cell* 75: 791-803 and in Rossi *et al.*, 1997, *Proc. Natl. Acad. Sci. USA* 94: 8405-8410, all of which are incorporated by reference herein) to identify polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction.

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The proteins provided by the present invention can similarly be used in assay to determine biological activity, including in a panel of multiple proteins for high-throughput screening; to raise antibodies or to elicit another immune response; as a reagent (including the labeled reagent) in assays designed to quantitatively determine levels of the protein (or its receptor) in biological fluids; as markers for tissues in which the corresponding protein is preferentially expressed (either constitutively or at a particular stage of tissue differentiation or development or in a disease state); and, of course, to isolate correlative receptors or ligands. Where the protein binds or potentially binds to another protein (such as, for example, in a receptor-ligand interaction), the protein can be used to identify the other protein with which binding occurs or to identify inhibitors of the binding interaction. Proteins involved in these binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction.

Any or all of these research utilities are capable of being developed into reagent grade or kit format for commercialization as research products.

Methods for performing the uses listed above are well known to those skilled in the art. References disclosing such methods include without limitation "Molecular Cloning: A Laboratory Manual", 2d ed., Cold Spring Harbor Laboratory Press, Sambrook, J., E.F. Fritsch and T. Maniatis eds., 1989, and "Methods in Enzymology: Guide to Molecular Cloning Techniques", Academic Press, Berger, S.L. and A.R. Kimmel eds., 1987.

#### Nutritional Uses

Polynucleotides and proteins of the present invention can also be used as nutritional sources or supplements. Such uses include without limitation use as a protein or amino acid supplement, use as a carbon source, use as a nitrogen source and use as a source of carbohydrate. In such cases the protein or polynucleotide of the invention can be added to the feed of a particular organism or can be administered as a separate solid or liquid preparation, such as in the form of powder, pills, solutions, suspensions or capsules. In the case of microorganisms, the protein or polynucleotide of the invention can be added to the medium in or on which the microorganism is cultured.

#### Cytokine and Cell Proliferation/Differentiation Activity

A protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may



induce production of other cytokines in certain cell populations. Many protein factors discovered to date, including all known cytokines, have exhibited activity in one or more factor-dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D, DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 10        Assays for T-cell or thymocyte proliferation include without limitation those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., *J. Immunol.* 137:3494-3500, 1986; Bertagnolli et al., *J. Immunol.* 145:1706-1712, 1990; Bertagnolli et al., *Cellular Immunology* 133:327-341, 1991; Bertagnolli, et al., *J. Immunol.* 149:3778-3783, 1992; Bowman et al., *J. Immunol.* 152: 1756-1761, 1994.

- 20        Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or thymocytes include, without limitation, those described in: Polyclonal T cell stimulation, Kruisbeek, A.M. and Shevach, E.M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.12.1-3.12.14, John Wiley and Sons, Toronto. 1994; and Measurement of mouse and human Interferon  $\gamma$ , Schreiber, R.D. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.8.1-6.8.8, John Wiley and Sons, Toronto. 1994.

- 25        Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells include, without limitation, those described in: Measurement of Human and Murine Interleukin 2 and Interleukin 4, Bottomly, K., Davis, L.S. and Lipsky, P.E. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto. 1991; deVries et al., *J. Exp. Med.* 173:1205-1211, 1991; Moreau et al., *Nature* 336:690-692, 1988; Greenberger et al., *Proc. Natl. Acad. Sci. U.S.A.* 80:2931-2938, 1983; Measurement of mouse and human interleukin 6 - Nordan, R. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.6.1-6.6.5, John Wiley and Sons, Toronto. 1991; Smith et al., *Proc. Natl. Acad. Sci. U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11 - Bennett, F., Giannotti, J., Clark, S.C. and Turner, K. J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto. 1991;

Measurement of mouse and human Interleukin 9 - Ciarletta, A., Giannotti, J., Clark, S.C. and Turner, K.J. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto. 1991.

Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and cytokine production) include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function; Chapter 6, Cytokines and their cellular receptors; Chapter 7, Immunologic studies in Humans); Weinberger et al., Proc. Natl. Acad. Sci. USA 77:6091-6095, 1980; Weinberger et al., Eur. J. Immun. 11:405-411, 1981; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988.

#### Immune Stimulating or Suppressing Activity

A protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), e.g., in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by viral (e.g., HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases caused by viral, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania spp., malaria spp. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, i.e., in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitis, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease.

Such a protein of the present invention may also be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to regulate immune responses in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response. The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or anergy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon reexposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as , for example, B7)), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to anergize the T cells, thereby inducing tolerance in a subject. Induction of long-term

tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of a combination of B lymphocyte antigens.

5           The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as  
10       described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc. Natl. Acad. Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

15           Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and autoantibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms.  
20       Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of autoantibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from  
25       the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythmatosis in MRL/*lpr/lpr* mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and  
30       murine experimental myasthenia gravis (see Paul ed., Fundamental Immunology, Raven Press, New York, 1989, pp. 840-856).

          Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune

response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic viral diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the patient. Another method of enhancing anti-viral immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (*e.g.*, sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (*e.g.*, a cytoplasmic-domain truncated portion) of an MHC class I  $\alpha$  chain protein and  $\beta_2$

microglobulin protein or an MHC class II  $\alpha$  chain protein and an MHC class II  $\beta$  chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated  
5 immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor specific immunity. Thus, the induction of a T cell mediated  
10 immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for thymocyte or splenocyte cytotoxicity include, without  
15 limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al.,  
20 J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Herrmann et al., Proc. Natl. Acad. Sci. USA 78:2488-2492, 1981; Herrmann et al., J. Immunol. 128:1968-1974, 1982; Handa et al., J. Immunol. 135:1564-1572, 1985; Takai et al., J. Immunol. 137:3494-3500, 1986; Bowman et al., J. Virology 61:1992-1998; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnoli et al.,  
25 Cellular Immunology 133:327-341, 1991; Brown et al., J. Immunol. 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, J. Immunol. 144:3028-3033, 1990; and Assays for B cell function: *In vitro*  
30 antibody production, Mond, J.J. and Brunswick, M. In *Current Protocols in Immunology*. J.E.e.a. Coligan eds. Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto. 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins that generate predominantly Th1 and CTL responses) include, without limitation, those described in: Current Protocols in Immunology, Ed by J. E. Coligan, A.M. Kruisbeek,

D.H. Margulies, E.M. Shevach, W Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 3, In Vitro assays for Mouse Lymphocyte Function 3.1-3.19; Chapter 7, Immunologic studies in Humans); Takai et al., J. Immunol. 137:3494-3500, 1986; Takai et al., J. Immunol. 140:508-512, 1988; Bertagnolli et al., J. Immunol. 149:3778-3783, 1992.

5 Dendritic cell-dependent assays (which will identify, among others, proteins expressed by dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery et al., J. Immunol. 134:536-544, 1995; Inaba et al., Journal of Experimental Medicine 173:549-559, 1991; Macatonia et al., Journal of Immunology 154:5071-5079, 1995; Porgador et al., Journal of Experimental Medicine 182:255-260, 1995; 10 Nair et al., Journal of Virology 67:4062-4069, 1993; Huang et al., Science 264:961-965, 1994; Macatonia et al., Journal of Experimental Medicine 169:1255-1264, 1989; Bhardwaj et al., Journal of Clinical Investigation 94:797-807, 1994; and Inaba et al., Journal of Experimental Medicine 172:631-640, 1990.

Assays for lymphocyte survival/apoptosis (which will identify, among others, 15 proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz et al., Cytometry 13:795-808, 1992; Gorczyca et al., Leukemia 7:659-670, 1993; Gorczyca et al., Cancer Research 53:1945-1951, 1993; Itoh et al., Cell 66:233-243, 1991; Zacharchuk, Journal of Immunology 145:4037-4045, 1990; Zamai et al., Cytometry 14:891-897, 1993; 20 Gorczyca et al., International Journal of Oncology 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica et al., Blood 84:111-117, 1994; Fine et al., Cellular Immunology 155:111-122, 1994; Galy et al., Blood 85:2770-2778, 1995; Toki et al., Proc. Nat. Acad Sci. USA 88:7548-7551, 1991.

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#### Hematopoiesis Regulating Activity

A protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell 30 lines indicates involvement in regulating hematopoiesis, e.g. in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid

cells such as granulocytes and monocytes/macrophages (i.e., traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either *in-vivo* or *ex-vivo* (i.e., in conjunction with bone marrow transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson et al. *Cellular Biology* 15:141-151, 1995; Keller et al., *Molecular and Cellular Biology* 13:473-486, 1993; McClanahan et al., *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, M.G. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 265-268, Wiley-Liss, Inc., New York, NY. 1994; Hirayama et al., *Proc. Natl. Acad. Sci. USA* 89:5907-5911, 1992; Primitive hematopoietic colony forming cells with high proliferative potential, McNiece, I.K. and Briddell, R.A. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 23-39, Wiley-Liss, Inc., New York, NY. 1994; Neben et al., *Experimental Hematology* 22:353-359, 1994; Cobblestone area forming cell assay, Ploemacher, R.E. In *Culture of Hematopoietic Cells*. R.I. Freshney, et al. eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, NY. 1994; Long term bone marrow cultures in the presence of stromal cells, Spooncer, E., Dexter, M. and



Allen, T. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 163-179, Wiley-Liss, Inc., New York, NY. 1994; Long term culture initiating cell assay, Sutherland, H.J. In *Culture of Hematopoietic Cells*. R.I. Freshney, *et al.* eds. Vol pp. 139-162, Wiley-Liss, Inc., New York, NY. 1994.

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#### Tissue Growth Activity

A protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for wound healing and tissue repair and replacement, and in the treatment of burns,  
10 incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation employing a protein of the invention may have prophylactic use in closed as  
15 well as open fracture reduction and also in the improved fixation of artificial joints. *De novo* bone formation induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

A protein of this invention may also be used in the treatment of periodontal  
20 disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue  
25 destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in  
30 circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and

in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The compositions of the invention may also be useful in the treatment of tendinitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation

of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium ).

Assays for wound healing activity include, without limitation, those described in: Winter, Epidermal Wound Healing, pps. 71-112 (Maibach, HI and Rovee, DT, eds.), Year Book Medical Publishers, Inc., Chicago, as modified by Eaglstein and Mertz, J. Invest. Dermatol 71:382-84 (1978).

#### Activin/Inhibin Activity

A protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin  $\alpha$  family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin- $\beta$  group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, United States Patent 4,798,885. A protein of the invention may also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for activin/inhibin activity include, without limitation, those described in: Vale et al., *Endocrinology* 91:562-572, 1972; Ling et al., *Nature* 321:779-782, 1986; Vale et al., *Nature* 321:776-779, 1986; Mason et al., *Nature* 318:659-663, 1985; Forage et al., *Proc. Natl. Acad. Sci. USA* 83:3091-3095, 1986.

#### Chemotactic/Chemokinetic Activity

A protein of the present invention may have chemotactic or chemokinetic activity (e.g., act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of wounds and other trauma to tissues, as well as in treatment of localized infections. For example, attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population. Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: *Current Protocols in Immunology*, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 6.12, Measurement of alpha and beta Chemokines 6.12.1-6.12.28; Taub et al. *J. Clin. Invest.* 95:1370-1376, 1995; Lind et al.

APMIS 103:140-146, 1995; Muller et al Eur. J. Immunol. 25: 1744-1748; Gruber et al. J. of Immunol. 152:5860-5867, 1994; Johnston et al. J. of Immunol. 153: 1762-1768, 1994.

#### Hemostatic and Thrombolytic Activity

5 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting  
10 formation of thromboses and for treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (e.g., stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

15 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet et al., J. Clin. Pharmacol. 26:131-140, 1986; Burdick et al., Thrombosis Res. 45:413-419, 1987; Humphrey et al., Fibrinolysis 5:71-79 (1991); Schaub, Prostaglandins 35:467-474, 1988.

#### Receptor/Ligand Activity

20 A protein of the present invention may also demonstrate activity as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and their ligands, receptor phosphatases and their ligands,  
25 receptors involved in cell-cell interactions and their ligands (including without limitation, cellular adhesion molecules (such as selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation, antigen recognition and development of cellular and humoral immune responses). Receptors and ligands are also useful for screening of potential peptide or small molecule inhibitors of the relevant  
30 receptor/ligand interaction. A protein of the present invention (including, without limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of receptor/ligand interactions.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Suitable assays for receptor-ligand activity include without limitation those described in: Current Protocols in Immunology, Ed by J.E. Coligan, A.M. Kruisbeek, D.H. Margulies, E.M. Shevach, W. Strober, Pub. Greene Publishing Associates and Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions 7.28.1-7.28.22), Takai et al., Proc. Natl. Acad. Sci. USA 84:6864-6868, 1987; Bierer et al., J. Exp. Med. 168:1145-1156, 1988; Rosenstein et al., J. Exp. Med. 169:149-160 1989; Stoltenborg et al., J. Immunol. Methods 175:59-68, 1994; Stitt et al., Cell 80:661-670, 1995.

#### 10 Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the inflammatory response, by inhibiting or promoting cell-cell interactions (such as, for example, cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production of other factors which more directly inhibit or promote an inflammatory response. Proteins exhibiting such activities can be used to treat inflammatory conditions including chronic or acute conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

25

#### Cadherin/Tumor Invasion Suppressor Activity

Cadherins are calcium-dependent adhesion molecules that appear to play major roles during development, particularly in defining specific cell types. Loss or alteration of normal cadherin expression can lead to changes in cell adhesion properties linked to tumor growth and metastasis. Cadherin malfunction is also implicated in other human diseases, such as pemphigus vulgaris and pemphigus foliaceus (auto-immune blistering skin diseases), Crohn's disease, and some developmental abnormalities.

The cadherin superfamily includes well over forty members, each with a distinct pattern of expression. All members of the superfamily have in common conserved

extracellular repeats (cadherin domains), but structural differences are found in other parts of the molecule. The cadherin domains bind calcium to form their tertiary structure and thus calcium is required to mediate their adhesion. Only a few amino acids in the first cadherin domain provide the basis for homophilic adhesion; modification of this recognition site can change the specificity of a cadherin so that instead of recognizing only  
5 itself, the mutant molecule can now also bind to a different cadherin. In addition, some cadherins engage in heterophilic adhesion with other cadherins.

E-cadherin, one member of the cadherin superfamily, is expressed in epithelial cell types. Pathologically, if E-cadherin expression is lost in a tumor, the malignant cells  
10 become invasive and the cancer metastasizes. Transfection of cancer cell lines with polynucleotides expressing E-cadherin has reversed cancer-associated changes by returning altered cell shapes to normal, restoring cells' adhesiveness to each other and to their substrate, decreasing the cell growth rate, and drastically reducing anchorage-independent cell growth. Thus, reintroducing E-cadherin expression reverts carcinomas  
15 to a less advanced stage. It is likely that other cadherins have the same invasion suppressor role in carcinomas derived from other tissue types. Therefore, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to treat cancer. Introducing such proteins or polynucleotides into cancer cells can reduce or eliminate the cancerous changes observed  
20 in these cells by providing normal cadherin expression.

Cancer cells have also been shown to express cadherins of a different tissue type than their origin, thus allowing these cells to invade and metastasize in a different tissue in the body. Proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be substituted in these cells for the  
25 inappropriately expressed cadherins, restoring normal cell adhesive properties and reducing or eliminating the tendency of the cells to metastasize.

Additionally, proteins of the present invention with cadherin activity, and polynucleotides of the present invention encoding such proteins, can be used to generate antibodies recognizing and binding to cadherins. Such antibodies can be used to block  
30 the adhesion of inappropriately expressed tumor-cell cadherins, preventing the cells from forming a tumor elsewhere. Such an anti-cadherin antibody can also be used as a marker for the grade, pathological type, and prognosis of a cancer, i.e. the more progressed the cancer, the less cadherin expression there will be, and this decrease in cadherin expression can be detected by the use of a cadherin-binding antibody.

Fragments of proteins of the present invention with cadherin activity, preferably a polypeptide comprising a decapeptide of the cadherin recognition site, and polynucleotides of the present invention encoding such protein fragments, can also be used to block cadherin function by binding to cadherins and preventing them from binding in ways that produce undesirable effects. Additionally, fragments of proteins of the present invention with cadherin activity, preferably truncated soluble cadherin fragments which have been found to be stable in the circulation of cancer patients, and polynucleotides encoding such protein fragments, can be used to disturb proper cell-cell adhesion.

Assays for cadherin adhesive and invasive suppressor activity include, without limitation, those described in: Hortsch et al. J Biol Chem 270 (32): 18809-18817, 1995; Miyaki et al. Oncogene 11: 2547-2552, 1995; Ozawa et al. Cell 63: 1033-1038, 1990.

#### Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via antibody-dependent cell-mediated cytotoxicity (ADCC)). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

#### Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s);



effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

### **ADMINISTRATION AND DOSING**

A protein of the present invention (from whatever source derived, including without limitation from recombinant and non-recombinant sources) may be used in a pharmaceutical composition when combined with a pharmaceutically acceptable carrier. Such a composition may also contain (in addition to protein and a carrier) diluents, fillers, salts, buffers, stabilizers, solubilizers, and other materials well known in the art. The term "pharmaceutically acceptable" means a non-toxic material that does not interfere with the effectiveness of the biological activity of the active ingredient(s). The characteristics of the carrier will depend on the route of administration. The pharmaceutical composition of the invention may also contain cytokines, lymphokines, or other hematopoietic factors such as M-CSF, GM-CSF, TNF, IL-1, IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8, IL-9, IL-10, IL-11, IL-12, IL-13, IL-14, IL-15, IFN, TNF0, TNF1, TNF2, G-CSF, Meg-CSF, thrombopoietin, stem cell factor, and erythropoietin. The pharmaceutical composition may further contain other agents which either enhance the activity of the protein or compliment its activity or use in treatment. Such additional factors and/or agents may be included in the pharmaceutical composition to produce a synergistic effect with protein of the invention, or to minimize side effects. Conversely, protein of the present invention may be included in formulations of the particular cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent to minimize side effects of the cytokine, lymphokine, other hematopoietic factor, thrombolytic or anti-thrombotic factor, or anti-inflammatory agent.

A protein of the present invention may be active in multimers (e.g., heterodimers or homodimers) or complexes with itself or other proteins. As a result, pharmaceutical

compositions of the invention may comprise a protein of the invention in such multimeric or complexed form.

The pharmaceutical composition of the invention may be in the form of a complex of the protein(s) of present invention along with protein or peptide antigens. The protein and/or peptide antigen will deliver a stimulatory signal to both B and T lymphocytes. B lymphocytes will respond to antigen through their surface immunoglobulin receptor. T lymphocytes will respond to antigen through the T cell receptor (TCR) following presentation of the antigen by MHC proteins. MHC and structurally related proteins including those encoded by class I and class II MHC genes on host cells will serve to present the peptide antigen(s) to T lymphocytes. The antigen components could also be supplied as purified MHC-peptide complexes alone or with co-stimulatory molecules that can directly signal T cells. Alternatively antibodies able to bind surface immunoglobulin and other molecules on B cells as well as antibodies able to bind the TCR and other molecules on T cells can be combined with the pharmaceutical composition of the invention.

The pharmaceutical composition of the invention may be in the form of a liposome in which protein of the present invention is combined, in addition to other pharmaceutically acceptable carriers, with amphipathic agents such as lipids which exist in aggregated form as micelles, insoluble monolayers, liquid crystals, or lamellar layers in aqueous solution. Suitable lipids for liposomal formulation include, without limitation, monoglycerides, diglycerides, sulfatides, lysolecithin, phospholipids, saponin, bile acids, and the like. Preparation of such liposomal formulations is within the level of skill in the art, as disclosed, for example, in U.S. Patent No. 4,235,871; U.S. Patent No. 4,501,728; U.S. Patent No. 4,837,028; and U.S. Patent No. 4,737,323, all of which are incorporated herein by reference.

As used herein, the term "therapeutically effective amount" means the total amount of each active component of the pharmaceutical composition or method that is sufficient to show a meaningful patient benefit, i.e., treatment, healing, prevention or amelioration of the relevant medical condition, or an increase in rate of treatment, healing, prevention or amelioration of such conditions. When applied to an individual active ingredient, administered alone, the term refers to that ingredient alone. When applied to a combination, the term refers to combined amounts of the active ingredients that result in the therapeutic effect, whether administered in combination, serially or simultaneously.

5 In practicing the method of treatment or use of the present invention, a therapeutically effective amount of protein of the present invention is administered to a mammal having a condition to be treated. Protein of the present invention may be administered in accordance with the method of the invention either alone or in combination with other therapies such as treatments employing cytokines, lymphokines or other hematopoietic factors. When co-administered with one or more cytokines, lymphokines or other hematopoietic factors, protein of the present invention may be administered either simultaneously with the cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors, or sequentially. If administered sequentially, the attending physician will decide on the appropriate sequence of administering protein of the present invention in combination with cytokine(s), lymphokine(s), other hematopoietic factor(s), thrombolytic or anti-thrombotic factors.

15 Administration of protein of the present invention used in the pharmaceutical composition or to practice the method of the present invention can be carried out in a variety of conventional ways, such as oral ingestion, inhalation, topical application or cutaneous, subcutaneous, intraperitoneal, parenteral or intravenous injection. Intravenous administration to the patient is preferred.

20 When a therapeutically effective amount of protein of the present invention is administered orally, protein of the present invention will be in the form of a tablet, capsule, powder, solution or elixir. When administered in tablet form, the pharmaceutical composition of the invention may additionally contain a solid carrier such as a gelatin or an adjuvant. The tablet, capsule, and powder contain from about 5 to 95% protein of the present invention, and preferably from about 25 to 90% protein of the present invention. When administered in liquid form, a liquid carrier such as water, petroleum, oils of animal or plant origin such as peanut oil, mineral oil, soybean oil, or sesame oil, or synthetic oils may be added. The liquid form of the pharmaceutical composition may further contain physiological saline solution, dextrose or other saccharide solution, or glycols such as ethylene glycol, propylene glycol or polyethylene glycol. When administered in liquid form, the pharmaceutical composition contains from about 0.5 to 90% by weight of protein of the present invention, and preferably from about 1 to 50% protein of the present invention.

When a therapeutically effective amount of protein of the present invention is administered by intravenous, cutaneous or subcutaneous injection, protein of the present

invention will be in the form of a pyrogen-free, parenterally acceptable aqueous solution. The preparation of such parenterally acceptable protein solutions, having due regard to pH, isotonicity, stability, and the like, is within the skill in the art. A preferred pharmaceutical composition for intravenous, cutaneous, or subcutaneous injection should contain, in addition to protein of the present invention, an isotonic vehicle such as Sodium Chloride Injection, Ringer's Injection, Dextrose Injection, Dextrose and Sodium Chloride Injection, Lactated Ringer's Injection, or other vehicle as known in the art. The pharmaceutical composition of the present invention may also contain stabilizers, preservatives, buffers, antioxidants, or other additives known to those of skill in the art.

The amount of protein of the present invention in the pharmaceutical composition of the present invention will depend upon the nature and severity of the condition being treated, and on the nature of prior treatments which the patient has undergone. Ultimately, the attending physician will decide the amount of protein of the present invention with which to treat each individual patient. Initially, the attending physician will administer low doses of protein of the present invention and observe the patient's response. Larger doses of protein of the present invention may be administered until the optimal therapeutic effect is obtained for the patient, and at that point the dosage is not increased further. It is contemplated that the various pharmaceutical compositions used to practice the method of the present invention should contain about 0.01 µg to about 100 mg (preferably about 0.1mg to about 10 mg, more preferably about 0.1 µg to about 1 mg) of protein of the present invention per kg body weight.

The duration of intravenous therapy using the pharmaceutical composition of the present invention will vary, depending on the severity of the disease being treated and the condition and potential idiosyncratic response of each individual patient. It is contemplated that the duration of each application of the protein of the present invention will be in the range of 12 to 24 hours of continuous intravenous administration. Ultimately the attending physician will decide on the appropriate duration of intravenous therapy using the pharmaceutical composition of the present invention.

Protein of the invention may also be used to immunize animals to obtain polyclonal and monoclonal antibodies which specifically react with the protein. As used herein, the term "antibody" includes without limitation a polyclonal antibody, a monoclonal antibody, a chimeric antibody, a single-chain antibody, a CDR-grafted antibody, a humanized antibody, or fragments thereof which bind to the indicated protein.

Such term also includes any other species derived from an antibody or antibody sequence which is capable of binding the indicated protein.

Antibodies to a particular protein can be produced by methods well known to those skilled in the art. For example, monoclonal antibodies can be produced by generation of antibody-producing hybridomas in accordance with known methods (see for example, 5 Goding, 1983, *Monoclonal antibodies: principles and practice*, Academic Press Inc., New York; and Yokoyama, 1992, "Production of Monoclonal Antibodies" in *Current Protocols in Immunology*, Unit 2.5, Greene Publishing Assoc. and John Wiley & Sons). Polyclonal sera and antibodies can be produced by inoculation of a mammalian subject with the 10 relevant protein or fragments thereof in accordance with known methods. Fragments of antibodies, receptors, or other reactive peptides can be produced from the corresponding antibodies by cleavage of and collection of the desired fragments in accordance with known methods (see for example, Goding, *supra*; and Andrew et al., 1992, "Fragmentation of Immunoglobulins" in *Current Protocols in Immunology*, Unit 2.8, Greene Publishing 15 Assoc. and John Wiley & Sons). Chimeric antibodies and single chain antibodies can also be produced in accordance with known recombinant methods (see for example, 5,169,939, 5,194,594, and 5,576,184). Humanized antibodies can also be made from corresponding murine antibodies in accordance with well known methods (see for example, U.S. Patent Nos. 5,530,101, 5,585,089, and 5,693,762). Additionally, human antibodies may be 20 produced in non-human animals such as mice that have been genetically altered to express human antibody molecules (see for example Fishwild *et al.*, 1996, *Nature Biotechnology* **14**: 845-851; Mendez *et al.*, 1997, *Nature Genetics* **15**: 146-156 (erratum *Nature Genetics* **16**: 410); and U.S. Patents 5,877,397 and 5,625,126). Such antibodies may be obtained using either the entire protein or fragments thereof as an immunogen. The peptide 25 immunogens additionally may contain a cysteine residue at the carboxyl terminus, and are conjugated to a hapten such as keyhole limpet hemocyanin (KLH). Methods for synthesizing such peptides are known in the art, for example, as in R.P. Merrifield, J. Amer.Chem.Soc. **85**, 2149-2154 (1963); J.L. Krstenansky, *et al.*, FEBS Lett. **211**, 10 (1987).

Monoclonal antibodies binding to the protein of the invention may be useful 30 diagnostic agents for the immunodetection of the protein. Neutralizing monoclonal antibodies binding to the protein may also be useful therapeutics for both conditions associated with the protein and also in the treatment of some forms of cancer where

abnormal expression of the protein is involved. In the case of cancerous cells or leukemic cells, neutralizing monoclonal antibodies against the protein may be useful in detecting and preventing the metastatic spread of the cancerous cells, which may be mediated by the protein.

5 For compositions of the present invention which are useful for bone, cartilage, tendon or ligament regeneration, the therapeutic method includes administering the composition topically, systemically, or locally as an implant or device. When administered, the therapeutic composition for use in this invention is, of course, in a pyrogen-free, physiologically acceptable form. Further, the composition may desirably  
10 be encapsulated or injected in a viscous form for delivery to the site of bone, cartilage or tissue damage. Topical administration may be suitable for wound healing and tissue repair. Therapeutically useful agents other than a protein of the invention which may also optionally be included in the composition as described above, may alternatively or additionally, be administered simultaneously or sequentially with the composition in the  
15 methods of the invention. Preferably for bone and/or cartilage formation, the composition would include a matrix capable of delivering the protein-containing composition to the site of bone and/or cartilage damage, providing a structure for the developing bone and cartilage and optimally capable of being resorbed into the body. Such matrices may be formed of materials presently in use for other implanted medical  
20 applications.

The choice of matrix material is based on biocompatibility, biodegradability, mechanical properties, cosmetic appearance and interface properties. The particular application of the compositions will define the appropriate formulation. Potential matrices for the compositions may be biodegradable and chemically defined calcium  
25 sulfate, tricalciumphosphate, hydroxyapatite, polylactic acid, polyglycolic acid and polyanhydrides. Other potential materials are biodegradable and biologically well-defined, such as bone or dermal collagen. Further matrices are comprised of pure proteins or extracellular matrix components. Other potential matrices are nonbiodegradable and chemically defined, such as sintered hydroxapatite, bioglass, aluminates, or other  
30 ceramics. Matrices may be comprised of combinations of any of the above mentioned types of material, such as polylactic acid and hydroxyapatite or collagen and tricalciumphosphate. The bioceramics may be altered in composition, such as in calcium-aluminate-phosphate and processing to alter pore size, particle size, particle shape, and biodegradability.

Presently preferred is a 50:50 (mole weight) copolymer of lactic acid and glycolic acid in the form of porous particles having diameters ranging from 150 to 800 microns. In some applications, it will be useful to utilize a sequestering agent, such as carboxymethyl cellulose or autologous blood clot, to prevent the protein compositions  
5 from disassociating from the matrix.

A preferred family of sequestering agents is cellulosic materials such as alkylcelluloses (including hydroxyalkylcelluloses), including methylcellulose, ethylcellulose, hydroxyethylcellulose, hydroxypropylcellulose, hydroxypropylmethylcellulose, and carboxymethylcellulose, the most preferred being cationic salts of  
10 carboxymethylcellulose (CMC). Other preferred sequestering agents include hyaluronic acid, sodium alginate, poly(ethylene glycol), polyoxyethylene oxide, carboxyvinyl polymer and poly(vinyl alcohol). The amount of sequestering agent useful herein is 0.5-20 wt%, preferably 1-10 wt% based on total formulation weight, which represents the amount necessary to prevent desorption of the protein from the polymer matrix and to  
15 provide appropriate handling of the composition, yet not so much that the progenitor cells are prevented from infiltrating the matrix, thereby providing the protein the opportunity to assist the osteogenic activity of the progenitor cells.

In further compositions, proteins of the invention may be combined with other agents beneficial to the treatment of the bone and/or cartilage defect, wound, or tissue in  
20 question. These agents include various growth factors such as epidermal growth factor (EGF), platelet derived growth factor (PDGF), transforming growth factors (TGF- $\alpha$  and TGF- $\beta$ ), and insulin-like growth factor (IGF).

The therapeutic compositions are also presently valuable for veterinary applications. Particularly domestic animals and thoroughbred horses, in addition to  
25 humans, are desired patients for such treatment with proteins of the present invention.

The dosage regimen of a protein-containing pharmaceutical composition to be used in tissue regeneration will be determined by the attending physician considering various factors which modify the action of the proteins, e.g., amount of tissue weight desired to be formed, the site of damage, the condition of the damaged tissue, the size of  
30 a wound, type of damaged tissue (e.g., bone), the patient's age, sex, and diet, the severity of any infection, time of administration and other clinical factors. The dosage may vary with the type of matrix used in the reconstitution and with inclusion of other proteins in the pharmaceutical composition. For example, the addition of other known growth factors, such as IGF I (insulin like growth factor I), to the final composition, may also effect

the dosage. Progress can be monitored by periodic assessment of tissue/bone growth and/or repair, for example, X-rays, histomorphometric determinations and tetracycline labeling.

5 Polynucleotides of the present invention can also be used for gene therapy. Such polynucleotides can be introduced either *in vivo* or *ex vivo* into cells for expression in a mammalian subject. Polynucleotides of the invention may also be administered by other known methods for introduction of nucleic acid into a cell or organism (including, without limitation, in the form of viral vectors or naked DNA).

10 Cells may also be cultured *ex vivo* in the presence of proteins of the present invention in order to proliferate or to produce a desired effect on or activity in such cells. Treated cells can then be introduced *in vivo* for therapeutic purposes.

Patent and literature references cited herein are incorporated by reference as if fully set forth.



What is claimed is:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:
  - (a) the nucleotide sequence of SEQ ID NO:21;
  - (b) the nucleotide sequence of SEQ ID NO:21 from nucleotide 8 to nucleotide 2008;
  - (c) the nucleotide sequence of the full-length protein coding sequence of clone er311\_20 deposited under accession number ATCC 98781;
  - (d) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
  - (e) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:22;
  - (f) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22;
  - (g) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d); and
  - (h) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(d), and that has a length that is at least 25% of the length of SEQ ID NO:21.
2. The polynucleotide of claim 1 wherein said polynucleotide is operably linked to at least one expression control sequence.
3. A host cell transformed with the polynucleotide of claim 2.
4. The host cell of claim 3, wherein said cell is a mammalian cell.
5. A process for producing a protein encoded by the polynucleotide of claim 2, which process comprises:

- (a) growing a culture of a host cell transformed with the polynucleotide of claim 2 in a suitable culture medium; and
- (b) purifying said protein from the culture.

6. A protein produced according to the process of claim 5.

7. An isolated polynucleotide encoding the protein of claim 6.

8. The polynucleotide of claim 7, wherein the polynucleotide comprises the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781.

9. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:22;
  - (b) a fragment of the amino acid sequence of SEQ ID NO:22, the fragment comprising eight contiguous amino acids of SEQ ID NO:22; and
  - (c) the amino acid sequence encoded by the cDNA insert of clone er311\_20 deposited under accession number ATCC 98781;
- the protein being substantially free from other mammalian proteins.

10. The protein of claim 9, wherein said protein comprises the amino acid sequence of SEQ ID NO:22.

11. A composition comprising the protein of claim 9 and a pharmaceutically acceptable carrier.

12. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of:

- (a) the nucleotide sequence of SEQ ID NO:65;
- (b) the nucleotide sequence of SEQ ID NO:65 from nucleotide 66 to nucleotide 827;
- (c) the nucleotide sequence of SEQ ID NO:65 from nucleotide 474 to nucleotide 827;

- (d) the nucleotide sequence of the full-length protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (e) a nucleotide sequence encoding the full-length protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (f) the nucleotide sequence of a mature protein coding sequence of clone d24\_1 deposited under accession number ATCC 98817;
- (g) a nucleotide sequence encoding a mature protein encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;
- (h) a nucleotide sequence encoding a protein comprising the amino acid sequence of SEQ ID NO:66;
- (i) a nucleotide sequence encoding a protein comprising a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66;
- (j) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 65 degrees C, or 4X SSC at 42 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g); and
- (k) the nucleotide sequence of a polynucleotide that hybridizes under conditions at least as stringent as 4X SSC at 50 degrees C, or 6X SSC at 40 degrees C with 50% formamide, to any one of the polynucleotides specified by (a)-(g), and that has a length that is at least 25% of the length of SEQ ID NO:65.

13. A protein comprising an amino acid sequence selected from the group consisting of:

- (a) the amino acid sequence of SEQ ID NO:66;
- (b) a fragment of the amino acid sequence of SEQ ID NO:66, the fragment comprising eight contiguous amino acids of SEQ ID NO:66; and
- (c) the amino acid sequence encoded by the cDNA insert of clone d24\_1 deposited under accession number ATCC 98817;

the protein being substantially free from other mammalian proteins.

## Abstract

Novel polynucleotides and the proteins encoded thereby are disclosed.

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Fig. 1A

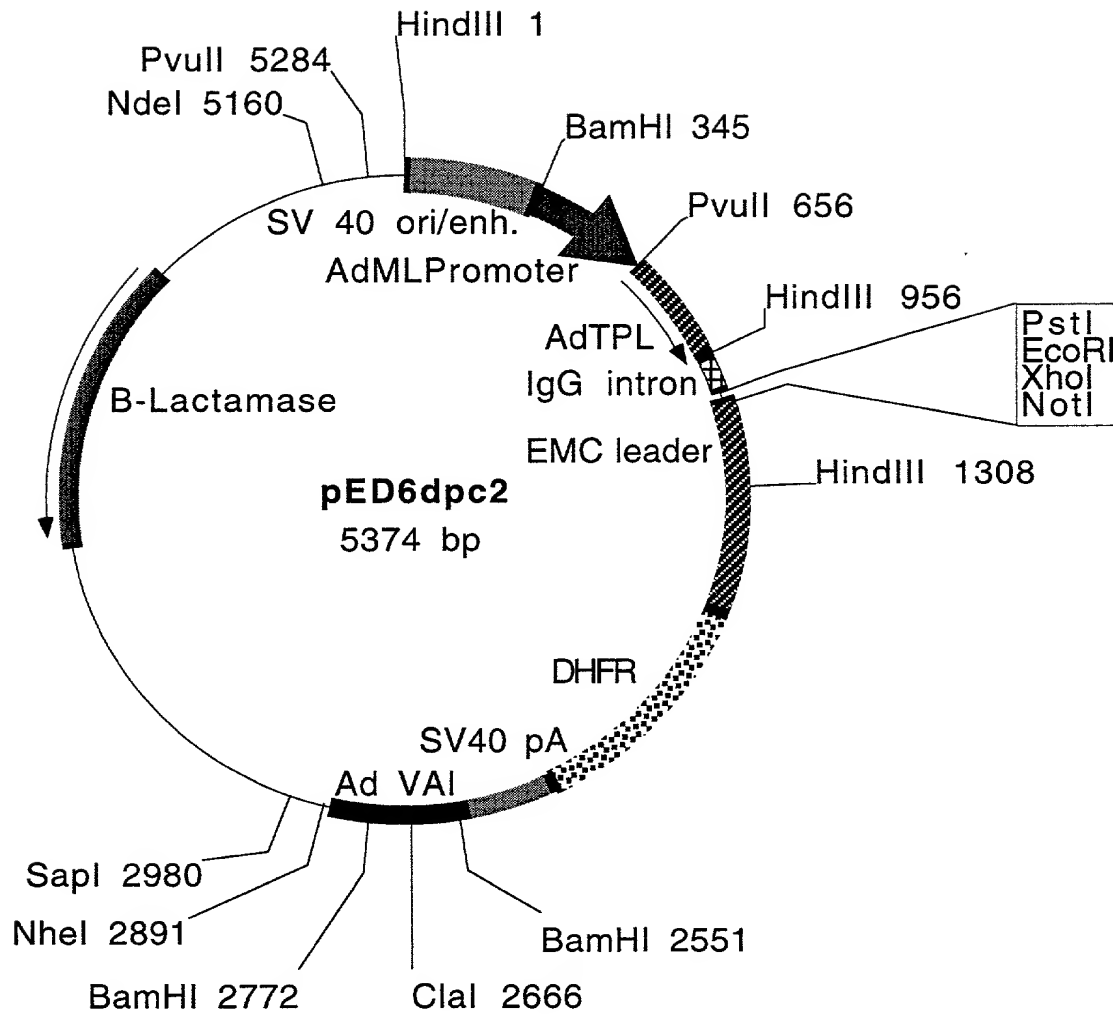
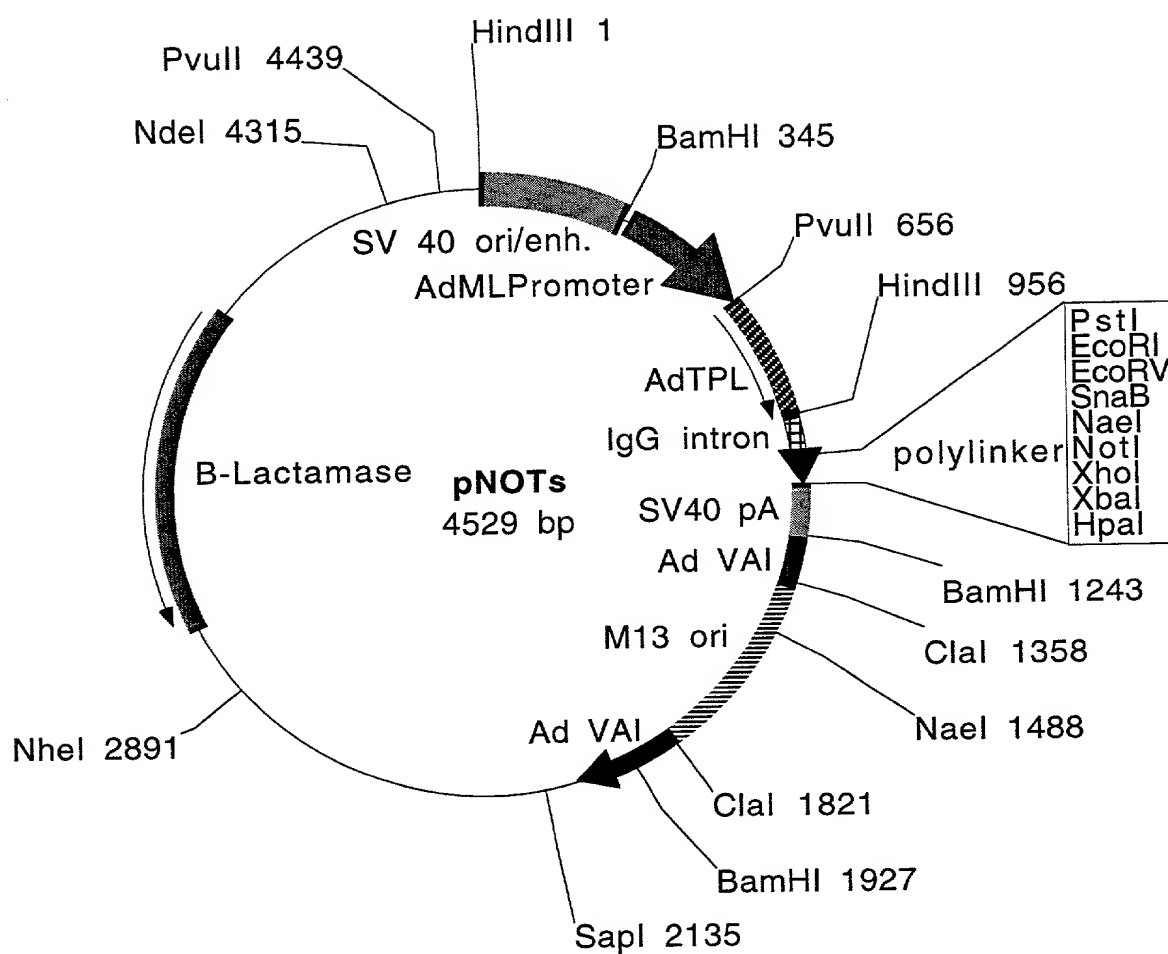


Fig. 1B



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 100 105 110  
 Ile Lys Lys Arg Ala Asn Lys Ala Ala Pro Glu Ile Asn Asn Leu Ile  
 115 120 125

Glu Glu Ala Thr Glu Phe Ile Lys Gln Asn Ile Val Ile Ser Ser Gly  
 130 135 140

Phe Val Gly Gly Phe Leu Leu Gly Leu Ala Ser  
 145 150 155

<210> 9  
 <211> 1850  
 <212> DNA  
 <213> Homo sapiens

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 <211> 206  
 <212> PRT  
 <213> Homo sapiens

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 Ala Cys Thr Cys Leu Leu Asp Pro Ser Thr Trp Arg Pro Ala His Val  
 35 40 45

Ser Gly Pro Ala Leu Ala Ser Ser Pro Gln Ile Leu Ser Val Phe Ser  
50 55 60

Leu Gly Phe Pro Gly Phe Val Asn Gly Ser Cys Val Ser Arg Tyr Lys  
65 70 75 80

Pro Asp Ile Ile Ser Pro Pro Gly Leu Pro Pro Pro Asp Leu Pro Ser  
85 90 95

Ser Val Ser Ile Phe Tyr Leu Gln Leu Leu Cys Ser His Gly His Cys  
100 105 110

Cys Ile Thr Glu Ser Gly Pro Leu Leu Ser Phe Ser Asn Trp Pro Pro  
115 120 125

Ser Leu Val Pro His Phe Leu Lys Ser Pro Val His Cys His Gln Ile  
130 135 140

Lys Leu Ser Pro Ala Arg Ser Pro Leu Ser Glu Lys Pro Pro Leu Thr  
145 150 155 160

Trp Lys His His Cys Leu Ala His Ile Leu Thr Tyr Ser Pro Ser Arg  
165 170 175

Leu Asp Pro His Thr Ser Phe Gln Pro Pro Leu Pro Leu His Ser Leu  
180 185 190

Leu Pro Pro Pro Pro Pro His Pro Leu Val Ser Pro Pro Leu  
195 200 205

<210> 11  
<211> 2216  
<212> DNA  
<213> Homo sapiens

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<210> 12  
 <211> 126  
 <212> PRT  
 <213> Homo sapiens

<400> 12  
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 20 25 30  
 Cys Val Leu Gln Val His Ala Ala Lys Val Ile Pro Ala His Pro Cys  
 35 40 45  
 Pro Val Ser Val Ser Phe Arg Val Ile Pro Tyr Leu Ser Ile Gly Gly  
 50 55 60  
 Leu Ile Leu Leu Asp Phe Leu Lys Thr Leu Arg Trp Ser Ile Arg Ser  
 65 70 75 80  
 Asp Phe Ser His Ser Ser Ala Gly Glu Leu Arg Ile Thr Ser Ser Phe  
 85 90 95  
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 100 105 110  
 Ser Leu Ile Gln Asn Ala Asn Lys Phe Asn Val Phe Leu Pro  
 115 120 125

<210> 13  
 <211> 1426  
 <212> DNA  
 <213> Homo sapiens

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 tttatttaag cctttctttg cttgtagggc attttgtatg tagagcagtt gaaaacagaa 360  
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<210> 14
<211> 80
<212> PRT
<213> Homo sapiens

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Ala Leu Ser Asp Pro Cys Thr Pro Leu Met Ser Pro Arg Arg Ala Ser
      20             25             30

Cys Ser Ser Pro Ser Ile Tyr Leu Ser Leu Ser Leu Leu Val Gly His
      35             40             45

Phe Val Cys Arg Ala Val Glu Asn Arg Thr Ser Glu Leu Asn Ile Cys
      50             55             60

Pro Asp Val Lys Val Leu Phe Met Thr Thr Leu Leu Ser Met Tyr Met
      65             70             75             80

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<210> 15
<211> 2364
<212> DNA
<213> Homo sapiens

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<210> 16  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 16  
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 Asn Ser Thr Val Ala Leu Ala Lys Val Arg Ser Phe Gly Thr Glu Asp  
 35 40 45  
 Arg Pro Thr Asp Arg Pro Ile Pro Pro Arg Asp Glu Val Phe Glu Tyr  
 50 55 60  
 Ile Ile Phe Arg Gly Ser Asp Ile Lys Asp Leu Thr Val Cys Glu Pro  
 65 70 75 80  
 Pro Lys Pro Gln Cys Ser Leu Pro Gln Asp Pro Ala Ile Val Gln Ser  
 85 90 95  
 Ser Leu Gly Ser Ser Thr Ser Ser Phe Gln Ser Met Gly Ser Tyr Gly  
 100 105 110  
 Pro Phe Gly Arg Met Pro Thr Tyr Ser Gln Phe Ser Pro Ser Ser Leu  
 115 120 125  
 Val Gly Gln Gln Phe Gly Ala Val Gly Val Ala Gly Ser Ser Leu Thr  
 130 135 140

Ser Phe Gly Thr Glu Thr Ser Asn Ser Gly Thr Leu Pro Gln Ser Ser  
 145 150 155 160  
 Ala Val Gly Ser Ala Phe Thr Gln Asp Thr Arg Ser Leu Lys Thr Gln  
 165 170 175  
 Leu Ser Gln Gly Arg Ser Ser Pro Gln Leu Asp Pro Leu Arg Lys Ser  
 180 185 190  
 Pro Thr Met Glu Gln Ala Val Gln Thr Ala Ser Ala His Leu Pro Ala  
 195 200 205  
 Pro Ala Ala Val Gly Arg Arg Ser Pro Val Ser Thr Arg Pro Leu Pro  
 210 215 220  
 Ser Ala Ser Gln Lys Ala Gly Glu Asn Gln Glu His Arg Gln Ala Glu  
 225 230 235 240  
 Val His Lys Val Ser Arg Pro Glu Asn Glu Gln Leu Arg Asn Asp Asn  
 245 250 255  
 Lys Arg Gln Val Ala Pro Gly Ala Pro Ser Ala Pro Arg Arg Gly Arg  
 260 265 270  
 Gly Gly His Arg Gly Gly Arg Gly Arg Phe Gly Ile Arg Arg Asp Gly  
 275 280 285  
 Pro Met Lys Phe Glu Lys Asp Phe Asp Phe Glu Ser Ala Asn Ala Gln  
 290 295 300  
 Phe Asn Lys Glu Glu Ile Asp Arg Glu Phe His Asn Lys Leu Lys Leu  
 305 310 315 320  
 Lys Glu Asp Lys Leu Glu Lys Gln Glu Lys Pro Val Asn Gly Glu Asp  
 325 330 335  
 Lys Gly Asp Ser Gly Val Asp Thr Gln Asn Ser Glu Gly Asn Ala Asp  
 340 345 350  
 Glu Glu Asp Pro Leu Gly Pro Asn Cys Tyr Tyr Asp Lys Thr Lys Ser  
 355 360 365  
 Phe Phe Asp Asn Ile Ser Cys Asp Asp Asn Arg Glu Arg Arg Pro Thr  
 370 375 380  
 Trp Ala Glu Glu Arg Arg Leu Asn Ala Glu Thr Phe Gly Ile Pro Leu  
 385 390 395 400  
 Arg Pro Asn Arg Gly Arg Gly Gly Tyr Arg Gly Arg Gly Gly Leu Gly  
 405 410 415  
 Phe Arg Gly Gly Arg Gly Arg Gly Gly Arg Gly Gly Thr Phe Thr  
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<210> 17  
 <211> 2760  
 <212> DNA  
 <213> Homo sapiens

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 ccatggacta agaacgatgc tggctttcaa gcaaaaaaga aaaataatca ttgtttattg 2400  
 tatactgcct ttttgaatc ctgtacaatt gcatcacggg tggggataaa aagaggaata 2460  
 ttctggttta tttcctagac tgttatttaa aaaaaaaaaa acatttgtgt aggacagcat 2520  
 ataaatgtaa taagtatcac actgtatata aacatatcaa tgtttgtcct gtataagaat 2580  
 tactaaatta caaatgcaat ttcattttaa cttctaggtt aagtttgagc ctgaaatttt 2640  
 aatgaagtgc aatactgagt gtgcctcatt atcttgcagc tgtaaacata ttggaatgta 2700  
 catgtcaata aaaccactgt acatttttat acagtgataa agtctaaaaa aaaaaaaaaa 2760

<210> 18  
 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 18

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 20 25 30  
 Ser Pro Arg Val Gln Arg Gln Val Thr Ser Leu Leu Arg Arg Val Leu  
 35 40 45  
 Pro Glu Val Thr Pro Ser Arg Leu Ala Ser Ile Ile Gly Val Lys Ser  
 50 55 60  
 Leu Pro Pro Ala Asp Ile Ser Asp Ile Ile His Ser Thr Glu Lys Gly  
 65 70 75 80  
 Asp Trp Asn Lys Leu Gly Ile Leu Asp Met Phe Leu Gly Cys Ile Ala  
 85 90 95  
 Lys Ala Leu Thr Val Gln Leu Lys Ala Lys Gly Thr Thr Ile Thr Gly  
 100 105 110  
 Thr Ala Gly Thr Thr Val Gly Lys Gly Val Thr Thr Val Thr Leu Pro  
 115 120 125  
 Met Ile Phe Asn Ser Ser Tyr Leu Arg Arg Gly Glu Ser His Trp Trp  
 130 135 140  
 Met Lys Gly Ser Thr Pro Thr Gln Ile Ser Glu Ile Ile Ile Lys Leu  
 145 150 155 160  
 Ile Lys Asp Met Ala Ala Gly His Leu Ser Glu Ala Trp Ser Arg Val  
 165 170 175  
 Thr Lys Asn Ala Ile Ala Glu Thr Ile Ile Ala Leu Thr Lys Met Glu  
 180 185 190  
 Glu Glu Phe Arg Ser Pro Val Arg Cys Ile Ala Thr Thr Arg Leu Trp  
 195 200 205  
 Leu Ala Leu Ala Ser Leu Cys Val Leu Asp Gln Asp His Val Asp Arg  
 210 215 220  
 Leu Ser Ser Gly Arg Trp Met Gly Lys Asp Gly Gln Gln Lys Gln Met  
 225 230 235 240  
 Pro Met Cys Asp Asn His Asp Asp Gly Glu Thr Ala Ala Ile Ile Leu  
 245 250 255  
 Cys Asn Val Cys Gly Asn Leu Cys Thr Asp Cys Asp Arg Phe Leu His  
 260 265 270  
 Leu His Arg Arg Thr Lys Thr His Gln Arg Gln Val Phe Lys Glu Glu  
 275 280 285  
 Glu Glu Ala Ile Lys Val Asp Leu His Glu Gly Cys Gly Arg Thr Lys  
 290 295 300  
 Leu Phe Trp Leu Met Ala Leu Ala Asp Ser Lys Thr Met Lys Ala Met  
 305 310 315 320

Val	Glu	Phe	Arg	Glu	His	Thr	Gly	Lys	Pro	Thr	Thr	Ser	Ser	Ser	Glu	325	330	335	
Ala	Cys	Arg	Phe	Cys	Gly	Ser	Arg	Ser	Gly	Thr	Glu	Leu	Ser	Ala	Val	340	345	350	
Gly	Ser	Val	Cys	Ser	Asp	Ala	Asp	Cys	Gln	Glu	Tyr	Ala	Lys	Ile	Ala	355	360	365	
Cys	Ser	Lys	Thr	His	Pro	Cys	Gly	His	Pro	Cys	Gly	Gly	Val	Lys	Asn	370	375	380	
Glu	Glu	His	Cys	Leu	Pro	Cys	Leu	His	Gly	Cys	Asp	Lys	Ser	Ala	Thr	385	390	395	400
Ser	Leu	Lys	Gln	Asp	Ala	Asp	Asp	Met	Cys	Met	Ile	Cys	Phe	Thr	Glu	405	410	415	
Ala	Leu	Ser	Ala	Ala	Pro	Ala	Ile	Gln	Leu	Asp	Cys	Ser	His	Ile	Phe	420	425	430	
His	Leu	Gln	Cys	Cys	Arg	Arg	Val	Leu	Glu	Asn	Arg	Trp	Leu	Gly	Pro	435	440	445	
Arg	Ile	Thr	Phe	Gly	Phe	Ile	Ser	Cys	Pro	Ile	Cys	Lys	Asn	Lys	Ile	450	455	460	
Asn	His	Ile	Val	Leu	Lys	Asp	Leu	Leu	Asp	Pro	Ile	Lys	Glu	Leu	Tyr	465	470	475	480
Glu	Asp	Val	Arg	Arg	Lys	Ala	Leu	Met	Arg	Leu	Glu	Tyr	Glu	Gly	Leu	485	490	495	
His	Lys	Ser	Glu	Ala	Ile	Thr	Thr	Pro	Gly	Val	Arg	Phe	Tyr	Asn	Asp	500	505	510	
Pro	Ala	Gly	Tyr	Ala	Met	Asn	Arg	Tyr	Ala	Tyr	Tyr	Val	Cys	Tyr	Lys	515	520	525	
Cys	Arg	Lys	Ala	Tyr	Phe	Gly	Gly	Glu	Ala	Arg	Cys	Asp	Ala	Glu	Ala	530	535	540	
Gly	Arg	Gly	Asp	Asp	Tyr	Asp	Pro	Arg	Glu	Leu	Ile	Cys	Gly	Ala	Cys	545	550	555	560
Ser	Asp	Val	Ser	Arg	Ala	Gln	Met	Cys	Pro	Lys	His	Gly	Thr	Asp	Phe	565	570	575	
Leu	Glu	Tyr	Lys	Cys	Arg	Tyr	Cys	Cys	Ser	Val	Ala	Val	Phe	Phe	Cys	580	585	590	
Phe	Gly	Thr	Thr	His	Phe	Cys	Asn	Ala	Cys	His	Asp	Asp	Phe	Gln	Arg	595	600	605	
Met	Thr	Ser	Ile	Pro	Lys	Glu	Glu	Leu	Pro	His	Cys	Pro	Ala	Gly	Pro	610	615	620	
Lys	Gly	Lys	Gln	Leu	Glu	Gly	Thr	Glu	Cys	Pro	Leu	His	Val	Val	His	625	630	635	640

Pro Pro Thr Gly Glu Glu Phe Ala Leu Gly Cys Gly Val Cys Arg Asn  
645 650 655

Ala His Thr Phe  
660

<210> 19  
<211> 1649  
<212> DNA  
<213> Homo sapiens

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atataaatat atctattttc tttttacaaa accagtttat aaatggtagg ggggtgtggg 180  
gcggacacat ggagctcccc ttgtgggggg gccccctcca ttaccgacc taccgccctt 240  
ttcctcacc cccacccccc tccccacccc ctggctgtga ctgctgtaag atgggggtat 300  
agaggctggg caattccccc cccctgttgt atagttggac tatgttataa cgcacaaaag 360  
agagctgacc ccaggggggag ccagagggtg atgggttcct tgcctccctt tccttccctt 420  
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gggtgaggcc ccaaacccct ctctggtagg gaaccgtggg gatgaagatg aagcttatat 540  
gcagttctct tctaggggct gtgggcaaag ggcattttgt aattaatatt ttcaagaatc 600  
agatgtctgg agttagggg tgggcttggg ggtggtggac gggcgggcct gctggagggg 660  
gagcttgggc cctgttgtag ttttaggttt gttttgttt tgttttgaat ttgggggggt 720  
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agctgcaaat gtttaagaga ataacagccc ccaactccac aggaaccgct gtaattaaat 840  
cagacagtag gaagactggg ctgctgccct caaagccaca gcccttgat gttccttttc 900  
cgagagcaga aggtctaggc tacagggagg gggagattgg ctcccgtgag tcaggctgtg 960  
tttggggctt gggccctggg attgggaaaa ggggatgggg cagactttgt aagcatatgc 1020  
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tataaactat aactcagacc caagctacaa ggttggaatt ttggttggtt ttttttttaa 1140  
gtaccctgcc tgtataattg catcagaatc cccaccccca ccccsgcc csgtgtttgt 1200  
attttgggtt ggtttactact cgcacatact cagttttcag ttttccctt tacagtcttc 1260  
tcccctcacc tccaggaccc tccccctttt taaaaaataa atcgtgaca agtgtgaatc 1320  
ccgtgaagac tttattttgt gttgtgtgta tcctgtacag caaggttggt ccttcgtaac 1380  
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gtccttggca tgttttgtat cagcgatcat tctgaactgt acatatattt gttgcgagag 1500  
gcaaagggca agttttggat tttgcttctt ccaagtttgt ttttaaacga caaataaaaa 1560  
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aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1649

<210> 20  
<211> 92  
<212> PRT  
<213> Homo sapiens

<400> 20  
Met Gly Glu Pro Ala Gly Gly Glu Asn Pro Pro Leu Ser Pro His Pro  
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Pro Gly Arg Ala Asn Val Lys Leu Leu Ile Phe Val Leu Tyr Ile Phe  
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Tyr Ile Asn Ile Ser Ile Phe Phe Leu Gln Asn Gln Phe Ile Asn Gly  
35 40 45  
Arg Gly Val Trp Gly Gly His Met Glu Leu Pro Leu Trp Gly Gly Pro  
50 55 60



Leu His Tyr Pro Thr Tyr Arg Pro Phe Pro His Pro Pro Pro His Ser  
65 70 75 80

Pro Pro Pro Gly Cys Asp Cys Cys Lys Met Gly Val  
85 90

<210> 21  
<211> 2644  
<212> DNA  
<213> Homo sapiens

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cagttcttca aaccctgagg aggtacagaa ggaaggggccc actgcgttgc aggactccaa 180  
ttctggggag cccgacatcc ctctctctca gccggactgc ggtgatttta ggagtctaca 240  
ggaggagcag tcgcgccccca cgacagcgggt ttcttccctt gccggtccag cccgggctcc 300  
cccctaccaag gagcctccat ggggtggccc tgccacagcc ccctacagct tagagaccct 360  
gaagggcggc actatccttg gcacccgtag cttgaaaggg acgagttact gccttttcgg 420  
gaggctgtct ggctgcgacg tgtgcctgga gcacccttcg gtgtctcggg accacgcagt 480  
gctgcagcac agggcgctcc gccctgacgg agaatgcgac agcaacgggc cgggcttcta 540  
cctctacagt ctgggaagca cccatggcac tttcttcaac aaaactcgca tcccacctcg 600  
cacctactgt cggatccacg ttgggctagt tgttcgcttt ggaggcagca cccggctctt 660  
tatctctcag ggaccagagg aagaccgaga ggcagaatcc gagttaacag taacacagtt 720  
gaaggaattg cgcaagcagc agcaaatatt gttggrgaag aagatgctag gagaagactc 780  
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tccaccgcc tcagcaaata tttgatgaaa aatgttgaaa gacggaatag attgatattc 2520  
atatagatat atgcatcaat taattctgta tttctatat atatatctta attacaaagg 2580  
gttatatgtt catttttagaa actatagatc atacataaaa gtccaaagga aaaaaaaaaa 2640  
aaaa 2644

<210> 22

<211> 667  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> UNSURE  
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<400> 22  
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 Ser Lys Ala Pro Ala Ser Ser Ser Ser Asn Pro Glu Glu Val Gln Lys  
 35 40 45  
 Glu Gly Pro Thr Ala Leu Gln Asp Ser Asn Ser Gly Glu Pro Asp Ile  
 50 55 60  
 Pro Pro Pro Gln Pro Asp Cys Gly Asp Phe Arg Ser Leu Gln Glu Glu  
 65 70 75 80  
 Gln Ser Arg Pro Thr Thr Ala Val Ser Ser Pro Gly Gly Pro Ala Arg  
 85 90 95  
 Ala Pro Pro Tyr Gln Glu Pro Pro Trp Gly Gly Pro Ala Thr Ala Pro  
 100 105 110  
 Tyr Ser Leu Glu Thr Leu Lys Gly Gly Thr Ile Leu Gly Thr Arg Ser  
 115 120 125  
 Leu Lys Gly Thr Ser Tyr Cys Leu Phe Gly Arg Leu Ser Gly Cys Asp  
 130 135 140  
 Val Cys Leu Glu His Pro Ser Val Ser Arg Tyr His Ala Val Leu Gln  
 145 150 155 160  
 His Arg Ala Ser Gly Pro Asp Gly Glu Cys Asp Ser Asn Gly Pro Gly  
 165 170 175  
 Phe Tyr Leu Tyr Asp Leu Gly Ser Thr His Gly Thr Phe Leu Asn Lys  
 180 185 190  
 Thr Arg Ile Pro Pro Arg Thr Tyr Cys Arg Val His Val Gly His Val  
 195 200 205  
 Val Arg Phe Gly Gly Ser Thr Arg Leu Phe Ile Leu Gln Gly Pro Glu  
 210 215 220  
 Glu Asp Arg Glu Ala Glu Ser Glu Leu Thr Val Thr Gln Leu Lys Glu  
 225 230 235 240  
 Leu Arg Lys Gln Gln Gln Ile Leu Leu Xaa Lys Lys Met Leu Gly Glu  
 245 250 255  
 Asp Ser Asp Glu Glu Glu Met Asp Thr Ser Glu Arg Lys Ile Asn  
 260 265 270

Ala Gly Ser Gln Asp Asp Glu Met Gly Cys Thr Trp Gly Met Gly Glu  
 275 280 285  
 Asp Ala Val Glu Asp Asp Ala Glu Glu Asn Pro Ile Val Leu Glu Phe  
 290 295 300  
 Gln Gln Glu Arg Glu Ala Phe Tyr Ile Lys Asp Pro Lys Lys Ala Leu  
 305 310 315 320  
 Gln Gly Phe Phe Asp Arg Glu Gly Glu Glu Leu Glu Tyr Glu Phe Asp  
 325 330 335  
 Glu Gln Gly His Ser Thr Trp Leu Cys Arg Val Arg Leu Pro Val Asp  
 340 345 350  
 Asp Ser Thr Gly Lys Gln Leu Val Ala Glu Ala Ile His Ser Gly Lys  
 355 360 365  
 Lys Lys Glu Ala Met Ile Gln Cys Ser Leu Glu Ala Cys Arg Ile Leu  
 370 375 380  
 Asp Thr Leu Gly Leu Leu Arg Gln Glu Ala Val Ser Arg Lys Arg Lys  
 385 390 395 400  
 Ala Lys Asn Trp Glu Asp Glu Asp Phe Tyr Asp Ser Asp Asp Asp Thr  
 405 410 415  
 Phe Leu Asp Arg Thr Gly Leu Ile Glu Lys Lys Arg Leu Asn Arg Met  
 420 425 430  
 Lys Lys Ala Gly Lys Ile Asp Glu Lys Pro Glu Thr Phe Glu Ser Leu  
 435 440 445  
 Val Ala Lys Leu Asn Asp Ala Glu Arg Glu Leu Ser Glu Ile Ser Glu  
 450 455 460  
 Arg Leu Lys Ala Ser Ser Gln Val Leu Ser Glu Ser Pro Ser Gln Asp  
 465 470 475 480  
 Ser Leu Asp Ala Phe Met Ser Glu Met Lys Ser Gly Ser Thr Leu Asp  
 485 490 495  
 Gly Val Ser Arg Lys Lys Leu His Leu Arg Thr Phe Glu Leu Arg Lys  
 500 505 510  
 Glu Gln Gln Arg Leu Lys Gly Leu Ile Lys Ile Val Lys Pro Ala Glu  
 515 520 525  
 Ile Pro Glu Leu Lys Lys Thr Glu Thr Gln Thr Thr Gly Ala Glu Asn  
 530 535 540  
 Lys Ala Lys Lys Leu Thr Leu Pro Leu Phe Gly Ala Met Lys Gly Gly  
 545 550 555 560  
 Ser Lys Phe Lys Leu Lys Thr Gly Thr Val Gly Lys Leu Pro Pro Lys  
 565 570 575  
 Arg Pro Glu Leu Pro Pro Thr Leu Met Arg Met Lys Asp Glu Pro Glu  
 580 585 590

Val Glu Glu Glu Glu Glu Glu Glu Glu Glu Glu Lys Glu Lys Glu  
595 600 605

Glu His Glu Lys Lys Lys Leu Glu Asp Gly Ser Leu Ser Arg Pro Gln  
610 615 620

Pro Glu Ile Glu Pro Glu Ala Ala Val Gln Glu Met Arg Pro Pro Thr  
625 630 635 640

Asp Leu Thr His Phe Lys Glu Thr Gln Thr His Gly Asn Ile Phe Leu  
645 650 655

Leu Leu Pro Val Leu Phe Ser Gly Gln Leu His  
660 665

<210> 23  
<211> 2402  
<212> DNA  
<213> Homo sapiens

<400> 23  
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cgggccggca gggccctgc ggtcggcaag ctggctcccc ggggtggccac cgggaccccc 180  
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gagcgcgagc gggaggggga gggagacgcg ggcggcgacg gactgggcag cagcctgtcg 360  
ctggccgtgc cccagggccc cctcagcttt gaggcgctgc tcgcccagggt gggggcgctg 420  
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gatcggaag actgagtagg gaaggcaggg ctgcccagaa gtctcagagg cacctcacgc 2160  
cagccatcgc ggagagctca gaggccgctc cccaccctgc ctctcctctg ctgctttgca 2220  
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ctgggctcca tctgcgccc aaagacatcc acccagacct cattatttct tgctctatca 2340  
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 aa 2402

<210> 24  
 <211> 520  
 <212> PRT  
 <213> Homo sapiens

<400> 24  
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 Tyr Gly Ala Phe Pro Pro Asn Ala Ser Gly Trp Glu Gln Pro Pro Asn  
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 Ala Ser Gly Val Ser Val Ala Ser Ala Ala Leu Ala Ala Ser Ala Ala  
 35 40 45  
 Ser Arg Val Ala Thr Ser Thr Asp Pro Ser Cys Ser Gly Phe Ala Pro  
 50 55 60  
 Pro Asp Phe Asn His Cys Leu Lys Asp Trp Asp Tyr Asn Gly Leu Pro  
 65 70 75 80  
 Val Leu Thr Thr Asn Ala Ile Gly Gln Trp Asp Leu Val Cys Asp Leu  
 85 90 95  
 Gly Trp Gln Val Ile Leu Glu Gln Ile Leu Phe Ile Leu Gly Phe Ala  
 100 105 110  
 Ser Gly Tyr Leu Phe Leu Gly Tyr Pro Ala Asp Arg Phe Gly Arg Arg  
 115 120 125  
 Gly Ile Val Leu Leu Thr Leu Gly Leu Val Gly Pro Cys Gly Val Gly  
 130 135 140  
 Gly Ala Ala Ala Gly Ser Ser Thr Gly Val Met Ala Leu Arg Phe Leu  
 145 150 155 160  
 Leu Gly Phe Leu Leu Ala Gly Val Asp Leu Gly Val Tyr Leu Met Arg  
 165 170 175  
 Leu Glu Leu Cys Asp Pro Thr Gln Arg Leu Arg Val Ala Leu Ala Gly  
 180 185 190  
 Glu Leu Val Gly Val Gly Gly His Phe Leu Phe Leu Gly Leu Ala Leu  
 195 200 205  
 Val Ser Lys Asp Trp Arg Phe Leu Gln Arg Met Ile Thr Ala Pro Cys  
 210 215 220  
 Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly Leu Phe Leu Glu Ser Ala  
 225 230 235 240  
 Arg Trp Leu Ile Val Lys Arg Gln Ile Glu Glu Ala Gln Ser Val Leu  
 245 250 255  
 Arg Ile Leu Ala Glu Arg Asn Arg Pro His Gly Gln Met Leu Gly Glu  
 260 265 270

Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu Asn Thr Cys Pro Leu Pro  
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 Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
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 His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
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 Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
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 Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
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Ala Thr Glu Asp Asp Leu Val Glu Met Gln Gly Tyr Lys Asp Lys Leu  
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Ser Ile Ile Gly Glu Val Leu Ser Arg Arg His Met Lys Val Ala Phe  
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Phe Gly Arg Thr Ser Ser Gly Lys Ser Ser Val Ile Asn Ala Met Leu  
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Trp Asp Lys Val Leu Pro Ser Gly Ile Gly His Ile Thr Asn Cys Phe  
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Leu Ser Val Glu Gly Thr Asp Gly Asp Lys Ala Tyr Leu Met Thr Glu  
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Gly Ser Asp Glu Lys Lys Ser Val Lys Thr Val Asn Gln Leu Ala His  
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Val Asp Ser Pro Gly Thr Asp Val Thr Thr Glu Leu Asp Ser Trp Ile  
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Asp Lys Phe Cys Leu Asp Ala Asp Val Phe Val Leu Val Ala Asn Ser  
195 200 205

Glu Ser Thr Leu Met Asn Thr Glu Lys His Phe Phe His Lys Val Asn  
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Glu Arg Leu Ser Lys Pro Asn Ile Phe Ile Leu Asn Asn Arg Trp Asp  
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Ala Ser Ala Ser Glu Pro Glu Tyr Met Glu Asp Val Arg Arg Gln His  
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Asn Ile Met Asp Ser Val Asn Leu Ala Ala Glu Asp Lys Arg His Tyr  
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Ser Val Glu Glu Arg Glu Asp Gln Ile Asp Arg Leu Asp Phe Ile Arg  
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Asn Gln Met Asn Leu Leu Thr Leu Asp Val Lys Lys Lys Ile Lys Glu  
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Val Thr Glu Glu Val Ala Asn Lys Val Ser Cys Ala Met Thr Asp Glu  
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Asp Ser Pro Asp Ser Asp Ser Ser Leu Ser Ser Pro Tyr Ser Thr Asp  
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Thr Leu Ser Ala Leu Arg Gly Asn Ser Gly Ser Val Leu Glu Gly Pro  
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Gly Arg Val Val Ala Asp Gly Thr Gly Thr Arg Thr Ile Ile Val Pro  
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Pro Leu Lys Thr Gln Leu Gly Asp Cys Thr Val Ala Thr Gln Ala Ser  
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Gly Leu Leu Ser Asn Lys Thr Lys Pro Val Ala Ser Val Ser Gly Gln  
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Ser Ala Ala Pro Thr Ser Gln Glu Arg Ser Ser Asn Pro Ala Pro Arg  
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Arg Gln Gln Ala Phe Val Ala Pro Leu Ser Gln Ala Pro Tyr Thr Phe  
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Gln His Gly Ser Pro Leu His Ser Thr Gly His Pro His Leu Ala Pro  
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Pro Ser Thr Leu Val His Gln Val Pro Val Ser Val Gly Pro Ser Leu  
595 600 605

Leu Thr Ser Ala Ser Val Ala Pro Ala Gln Tyr Gln His Gln Phe Ala  
610 615 620

Thr Gln Ser Tyr Ile Gly Ser Ser Arg Gly Ser Thr Ile Tyr Thr Gly  
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Tyr Pro Leu Ser Pro Thr Lys Ile Ser Gln Tyr Ser Tyr Leu  
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<210> 33

<211> 2731

<212> DNA  
<213> Homo sapiens

<220>  
<221> unsure  
<222> (2173)

<220>  
<221> unsure  
<222> (2700)

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<210> 34



<211> 441  
 <212> PRT  
 <213> Homo sapiens

<400> 34

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 20 25 30

Thr Val Ala Ala Ala Asp Arg Ser Lys Trp His Ile Pro Ile Pro Ser  
 35 40 45

Gly Lys Asn Tyr Phe Ser Phe Gly Lys Ile Leu Phe Arg Asn Thr Thr  
 50 55 60

Ile Phe Leu Lys Phe Asp Gly Glu Pro Cys Asp Leu Ser Leu Asn Ile  
 65 70 75 80

Thr Trp Tyr Leu Lys Ser Ala Asp Cys Tyr Asn Glu Ile Tyr Asn Phe  
 85 90 95

Lys Ala Glu Glu Val Glu Leu Tyr Leu Glu Lys Leu Lys Glu Lys Arg  
 100 105 110

Gly Leu Ser Gly Lys Tyr Gln Thr Ser Ser Lys Leu Phe Gln Asn Cys  
 115 120 125

Ser Glu Leu Phe Lys Thr Gln Thr Phe Ser Gly Asp Phe Met His Arg  
 130 135 140

Leu Pro Leu Leu Gly Glu Lys Gln Glu Ala Lys Glu Asn Gly Thr Asn  
 145 150 155 160

Leu Thr Phe Ile Gly Asp Lys Thr Ala Met His Glu Pro Leu Gln Thr  
 165 170 175

Trp Gln Asp Ala Pro Tyr Ile Phe Ile Val His Ile Gly Ile Ser Ser  
 180 185 190

Ser Lys Glu Ser Ser Lys Glu Asn Ser Leu Ser Asn Leu Phe Thr Met  
 195 200 205

Thr Val Glu Val Lys Gly Pro Tyr Glu Tyr Leu Thr Leu Glu Asp Tyr  
 210 215 220

Pro Leu Met Ile Phe Phe Met Val Met Cys Ile Val Tyr Val Leu Phe  
 225 230 235 240

Gly Val Leu Trp Leu Ala Trp Ser Ala Cys Tyr Trp Arg Asp Leu Leu  
 245 250 255

Arg Ile Gln Phe Trp Ile Gly Ala Val Ile Phe Leu Gly Met Leu Glu  
 260 265 270

Lys Ala Val Phe Tyr Ala Glu Phe Gln Asn Ile Arg His Lys Gly Glu  
 275 280 285

Ser Val Gln Gly Ala Leu Ile Leu Ala Glu Leu Leu Ser Ala Val Lys



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tcagaatgtg tctctctcat ctaatgtc tctgtttaat ggtgatgcct cgcgtacagg 1500
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<210> 36
<211> 164
<212> PRT
<213> Homo sapiens

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<400> 36
Met Gly Gly Met Val Arg Glu Glu Ala Leu Ala Trp Met Cys Arg Glu
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Pro Arg Lys Ala Phe Ser Ala Ile Val Gly Pro Ser Leu Gly Pro Asp
      20                      25                      30

Ser Thr Pro Gly Trp Gly Thr Gly Glu Trp Ala Thr Gly Gly Ala Ile
      35                      40                      45

Leu Gly Arg Pro Thr Pro Cys Ala Val Pro Gly Thr Gly Phe Ser Leu
      50                      55                      60

Leu Ser Thr Cys Ser Ser Pro Arg Gly Pro Val Pro Glu Thr Gly Arg
      65                      70                      75                      80

Gly Trp Arg Val Pro Thr Pro Cys Ser Leu Pro Asp Leu Leu Arg Asp
      85                      90                      95

Asp Asp Ala Val Cys Val Pro His Val Gly Pro Pro Pro Ala Cys His
      100                      105                      110

Leu Asn Ala Leu His Gly Pro Val Cys Gly Thr Gly Gly Gln Val Gln
      115                      120                      125

Trp Cys Ala Glu Leu His Trp Glu Asp Phe Gln Arg Gly Arg Ala Ala
      130                      135                      140

Gly Ile Leu Arg Trp Ile Asn Pro Ser Pro Pro Gly Arg Cys Gly Phe
      145                      150                      155                      160

Leu Val Gly Leu

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<210> 37
<211> 1493
<212> DNA
<213> Homo sapiens

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<220>
<221> unsure
<222> (1415)

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<400> 37
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gaccggcagc cggcaagatg cgaccgccct gccagcatg tctcaactt tctgggcggt 180
catgatcctg gccagcctgc tcatgccta ctgcagtcag ctggccgccc gcacctgtga 240
gattgtgacc ttggaccggg acagcagcca gctcggagg acgatcgccc ggcagaccgc 300

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ccgctgtgcg tgtagaaagg ggcagatcgc cggcaccacg agagcccggc ccgctgtgt 360
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<210> 38
<211> 132
<212> PRT
<213> Homo sapiens

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<400> 38
Met Ala Pro Ser Pro Arg Thr Gly Ser Arg Gln Asp Ala Thr Ala Leu
  1               5               10               15

Pro Ser Met Ser Ser Thr Phe Trp Ala Phe Met Ile Leu Ala Ser Leu
      20               25               30

Leu Ile Ala Tyr Cys Ser Gln Leu Ala Ala Gly Thr Cys Glu Ile Val
      35               40               45

Thr Leu Asp Arg Asp Ser Ser Gln Pro Arg Arg Thr Ile Ala Arg Gln
      50               55               60

Thr Ala Arg Cys Ala Cys Arg Lys Gly Gln Ile Ala Gly Thr Thr Arg
      65               70               75               80

Ala Arg Pro Ala Cys Val Asp Ala Arg Ile Ile Lys Thr Lys Gln Trp
      85               90               95

Cys Asp Met Leu Pro Cys Leu Glu Gly Glu Gly Cys Asp Leu Leu Ile
      100              105              110

Asn Arg Ser Gly Trp Thr Cys Thr Gln Pro Gly Gly Arg Ile Lys Thr
      115              120              125

Thr Thr Val Ser
      130

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<210> 39
<211> 3693
<212> DNA
<213> Homo sapiens

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<220>  
 <221> unsure  
 <222> (108)

<400> 39

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 <211> 230  
 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
 Val Glu Ala Val Ser Glu Gly Thr Asp Ser Gly Ile Ser Ala Glu Ala  
 50 55 60  
 Ala Gly Ile Asp Trp Gly Ile Phe Pro Glu Ser Asp Ser Lys Asp Pro  
 65 70 75 80  
 Gly Gly Asp Gly Ile Asp Trp Gly Asp Asp Ala Val Ala Leu Gln Ile  
 85 90 95  
 Thr Val Leu Glu Ala Gly Thr Gln Ala Pro Glu Gly Val Ala Arg Gly  
 100 105 110  
 Pro Asp Ala Leu Thr Leu Leu Glu Tyr Thr Glu Thr Arg Asn Gln Phe  
 115 120 125  
 Leu Asp Glu Leu Met Glu Leu Glu Ile Phe Leu Ala Gln Arg Ala Val  
 130 135 140  
 Glu Leu Ser Glu Glu Ala Asp Val Leu Ser Val Ser Gln Phe Gln Leu  
 145 150 155 160  
 Ala Pro Ala Ile Leu Gln Gly Gln Thr Lys Glu Lys Met Val Thr Met  
 165 170 175  
 Val Ser Val Leu Glu Asp Leu Ile Gly Lys Leu Thr Ser Leu Gln Leu  
 180 185 190  
 Gln His Leu Phe Met Ile Leu Ala Ser Pro Arg Ser Gly Phe Pro Leu  
 195 200 205  
 Met Gln Gly Ser Ala Ile Leu Ser Ser Ser Ala Ser Leu Tyr Ser Ser  
 210 215 220  
 Ser Cys Ser Met Thr Pro  
 225 230

<210> 41  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

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<210> 42  
 <211> 240  
 <212> PRT  
 <213> Homo sapiens

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 20 25 30  
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 35 40 45  
 Gly Thr Glu Cys Val Leu Ser Ser Thr Gly Arg Thr Ala Ala Cys Phe  
 50 55 60  
 Leu Pro Thr Ser Leu Leu Pro Thr Ser Pro Ala Ala Trp Leu Gly Pro  
 65 70 75 80  
 Glu Ala Leu Cys Leu Pro Gly Arg Pro Gly Thr Thr Gly Leu Arg Asp  
 85 90 95

Thr Gly Gly Pro Leu Leu Leu Pro Pro Pro Thr Leu Leu Gln Asp Thr  
 100 105 110  
 Thr Arg Trp Cys Trp Met Leu Val Leu Trp Pro Ala Lys Val His Gly  
 115 120 125  
 Asp Ser Pro His Gly Ile Leu Arg Asp Gln Ala Ala Gly Ile Gly Lys  
 130 135 140  
 Glu Phe His Pro Asp Arg Cys Pro Ser Gln Val Pro Arg Arg Pro His  
 145 150 155 160  
 His Thr Pro Phe Gln Gly Gln Gly Ser Ser Lys Pro Arg Ala Arg Ile  
 165 170 175  
 Leu Cys Cys Cys Leu Val Glu Ser Leu Pro Pro Cys Val Gly Ser Val  
 180 185 190  
 Gly Gln Ala Glu Cys Ile Gly Asp Arg Ala Val Ser Met Gly Leu Gly  
 195 200 205  
 Val Cys Glu Leu Arg Pro Arg Cys Ala Val Trp Arg Arg Val Leu Ser  
 210 215 220  
 Gly Lys Arg Cys Gly Phe Lys Val Cys Val Cys Arg Gly Trp Val Cys  
 225 230 235 240

<210> 43  
 <211> 1784  
 <212> DNA  
 <213> Homo sapiens

<400> 43  
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 cttgctgaat taaatatttt tgagtgggtc atttttaagt atagtgaaca agacaccata 180  
 ttaagtacag tgataaagca tctatattct gtataaaaaa aaaaaatctg cctatgcatg 240  
 ttttttaaga aaaaaaaaaat ggctgtatcg gcctgtatgg gactgtaatg cgcttagtgg 300  
 tctgacatat actggaaatg tatgtatact ggcgtacttt atattctcta aaatgcttaa 360  
 tgcctttgaa attttgtaat caaaaaaaag ctttgaaaaa tctaaagggg agagtattct 420  
 ttaaagtttt taacataagc ttgtcaatgc acatgtagat ggtagcatg tttagcaaac 480  
 cttgtgaaat tataataagt ttgtagttac atgtgaaact ctaaatgcat ggcaactgtt 540  
 aatgtcataa cagtttagtt attttgttct gttctgtcat gtgccacaaa atatgtactt 600  
 ttttcacttt tttccctttg tatatcagtt acgggttaca actggttcat tctgaaaaca 660  
 acaacaacaa aagtcatttc atatttttta acaattgtat aagtgcocaa gtaattcact 720  
 acagcctaaa gccttgccct tgtaatttga cttctgacat gttggcaatc aaagcatgca 780  
 cttgtaacaa tgaaaaagaa aaagcatttt atattactac tcaataaaat gtgcatgaac 840  
 ttacagaatt ctcatccttc cactgagtc gctgaaggga tttatgtgca caaccacat 900  
 gtgtcttcta ggtgctggcc caccaccaca catcacaggc tgatttccac aggtctcttc 960  
 ctaggggcct cgtgatctga ggggtggtgc ctacttccac tgtaagaaag aatcttggtg 1020  
 gatttgtgtc tcaaatcaga taagagaagc ctgttttaaag agcagatgcc atcttctggc 1080  
 ttctctaagg agccagttta aaaaccagag cattcctttt tattgaaaaa taaaattaat 1140  
 ttgttatcag gttgtttcag ttgtatttga tgccctatct atctgctaaa gcaaaaagta 1200  
 ctaggctact aagtgcattt tcatcacaga aaagagttgc atttgtatta acaagaaatt 1260  
 tgtataccca cgcttcagct actatctaact catcacccga agatttaaga tacaccaaat 1320  
 ttcagtttgt ttgtaacatt gtcatccttt agtgcacttt gttttatata ataaagtatg 1380  
 cctgttatat taaataataa gaatatggca attagcgata tagcataccc aaacaaagat 1440  
 gttctcgata cagtctggca aagactatcc caaggttatt ttaatgaatt cagacatttt 1500  
 ttctgtgga tattttctcca tctataaaaa agtggaacc aaggaaaata ttttagtgca 1560



acttactaga gtgatgatgt gaaagaaatg gtgattctgg tatcatgggtg tttattttct 1620  
 ttcttataac tgcagagaaa atactctgac taaaaaaaaat tcattttttt ggattccttt 1680  
 cttttacaaa ttgtgctgag gcaactatgg catagaaata aacatttgac attaaaataa 1740  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1784

<210> 44  
 <211> 82  
 <212> PRT  
 <213> Homo sapiens

<400> 44  
 Met Cys His Lys Ile Cys Thr Phe Phe Thr Phe Phe Pro Leu Tyr Ile  
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 Ser Tyr Gly Leu Gln Leu Val His Ser Glu Asn Asn Asn Asn Lys Ser  
 20 25 30  
 Pro Phe Ile Phe Phe Asn Asn Cys Ile Ser Ala Gln Val Ile His Tyr  
 35 40 45  
 Ser Leu Lys Pro Cys Leu Cys Asn Leu Thr Ser Asp Met Leu Ala Ile  
 50 55 60  
 Lys Ala Cys Thr Cys Asn Asn Glu Lys Glu Lys Ala Phe Tyr Ile Thr  
 65 70 75 80  
 Thr Gln

<210> 45  
 <211> 1034  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> (598)

<400> 45  
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 aggatctatc acaagctccg ttctcctggc cggcggggcg actggttagcg caggcttgtc 120  
 acgcggccac cgcgcccttg cacactcacc gcgaccacc gcacacagcc gcttacctcc 180  
 aagagctggg gcgcatgcmc aaagtggccc tcgagggccc agatgagacc accctaaagg 240  
 agctggccga gacctgcaa cagaagaaca ttgaccacat gctgtggctt gagcaaccag 300  
 agaatatcgc cacttgatt gctctccggc cctaccocaa ggaagaagtg ggccagtatt 360  
 tgaagaagtt ccgattgttc aagtaactgc tgctttgatg tgtttgaata cgcaggccac 420  
 ccattccaaa gcatcatgtg ttccctgcag tgtcagcttg ctcccgctt tcagttgtga 480  
 caatttcttg agggttaagc acatgttcat attaaagttg tcattaataa ctacttcctc 540  
 ttattaataa gttcaagtgg ggaaggtggg agagcagtat tgtctgggga tcattgcnc 600  
 aatagaagat ttggtttagac tctcctgtgg ggctcaagga aactcccttc cagtcactcg 660  
 ggtttgaac tttgcttttg aattccttct tattcacatc cagttatcat atttcattga 720  
 atccaagata acctcaactt caagatgcgg tagtatttta tgtattgtta aaaaatatgc 780  
 cggcaaatata aacacttgta tttcaataac aaagatgtta aaatttggcc agtgtgggtg 840  
 ctcacatctg ttaattccag ggttttggga agccaaggca ggaggatcgc ttgagcccat 900  
 gagttcaagg ttacagtcag ttctaatacag gccaccgcac tccagcgtgg gcaacagagt 960  
 gagacacggg ttctataaag attaataaca agttaaaaaa aaaaaaaaaa aaaaaaaaaa 1020  
 aaaaaaaaaa aaaa 1034

<210> 46

<211> 126  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 46  
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     1                    5                    10                    15  
 Leu Arg Lys Asp Leu Ser Gln Ala Pro Phe Ser Trp Pro Ala Gly Ala  
           20                    25                    30  
 Leu Val Ala Gln Ala Cys His Ala Ala Thr Ala Ala Leu His Thr His  
           35                    40                    45  
 Arg Asp His Pro His Thr Ala Ala Tyr Leu Gln Glu Leu Gly Arg Met  
           50                    55                    60  
 Arg Lys Val Val Leu Glu Ala Pro Asp Glu Thr Thr Leu Lys Glu Leu  
           65                    70                    75                    80  
 Ala Glu Thr Leu Gln Gln Lys Asn Ile Asp His Met Leu Trp Leu Glu  
                     85                    90                    95  
 Gln Pro Glu Asn Ile Ala Thr Cys Ile Ala Leu Arg Pro Tyr Pro Lys  
           100                    105                    110  
 Glu Glu Val Gly Gln Tyr Leu Lys Lys Phe Arg Leu Phe Lys  
           115                    120                    125

<210> 47  
 <211> 1626  
 <212> DNA  
 <213> Homo sapiens

<400> 47  
 caacttgtgt agctgaaggt ttgtttgtga cttattacag agcctgtgac ttaaaaatcc 60  
 ttcccacaac cacaagctaa agtgggagaa gacaaactac ctacaccttt caaccaagag 120  
 ggaggagcaa aaatcagtga acttttacag aagaacctgc cagcctgtga tgatcctacc 180  
 aaagagaaac ctcaatgagt tatggaattt ccttttttgt gaattgagt ctgtttttgc 240  
 ttttctcaga ttccaaatga gagtatacat tttcttttgt ttgatgtgct gggtgagatc 300  
 tgataataaa agaccatgcc ttgaattctc tcagctaagt gtaaaggatt ccttcagaga 360  
 tttatttatt ccgagaatag agaccattct gatgatgtat acaaggaaca acctaaactg 420  
 tgctgagcca ctgtttgaac aaaataactc acttaatgtt aatttcaaca cacaaaagaa 480  
 aacagtctgg cttattcacg gatacagacc agtaggctcc atcccattat ggcttcagaa 540  
 cttcgttaagg attttgctga atgaagaaga tatgaatgta attgtagtag actggagccg 600  
 ggggtgctaca acttttattt ataatagagc agttaaaaac accagaaaag ttgctgtgag 660  
 tttgagtgtg cacattaaaa atcttttgaa gcatggtgca tctcttgaca attttcattt 720  
 cataggtgtg agtttagggg ctcatatcag tggatttgtt ggaaagatat ttcatggtca 780  
 acttggaaga ataacaggtc ttgacctgc tgggccaagg ttctccagaa aaccaccata 840  
 tagcagatta gattacacgg atgcaaagtt tgtggatgtc atccattctg actccaatgg 900  
 aattcaattc attaaatgca accaccagag agcagttcac ttgttcattg catctttaga 960  
 aacaaactgc aatttttattt catttccttg tcgttcatac aaagattaca agactagctt 1020  
 atgtgtggac tgtgactgtt ttaaggaaaa atcatgtcct cggctgggtt atcaagccaa 1080  
 gctattttaa ggtgttttaa aagaaaggat ggaaggaaga cctcttagga cactgtgtt 1140  
 tttggataca agtgctattt attttgttct cagtataatt gttccagata aaactatgat 1200  
 ggatggctcg ttttcattta aattattaaa tcagcttgga atgattgaag agccaaggct 1260  
 ttatgaagaa agataacata tgtaaagag gcacccttac tctaaacaac tagtgacttt 1320  
 aaaagtctta agcgtatcag gagatggaga ccacctctgc taacatggtg aaacctgtc 1380  
 tctactaaaa attcagaaaa ttagctgggc atggtggcac gtgcctgtag tccagctac 1440

tcaggaggct gaggcaagag aattgcttga acccaggagg tggagggttgc agtgagctga 1500  
gattgcaccg ctgccctcca gcctgggtga cagagcaaga ctccatttca aataaataaa 1560  
taaataaata aataaataaa taaataaata aataaataaa gttaaagagt aaaaaaaaaa 1620  
aaaaaa 1626

<210> 48  
<211> 368  
<212> PRT  
<213> Homo sapiens

<400> 48  
Met Ile Leu Pro Lys Arg Asn Leu Asn Glu Leu Trp Asn Phe Leu Phe  
1 5 10 15  
Gly Glu Leu Ser Ala Val Phe Ala Phe Leu Arg Phe Gln Met Arg Val  
20 25 30  
Tyr Ile Phe Leu Cys Leu Met Cys Trp Val Arg Ser Asp Asn Lys Arg  
35 40 45  
Pro Cys Leu Glu Phe Ser Gln Leu Ser Val Lys Asp Ser Phe Arg Asp  
50 55 60  
Leu Phe Ile Pro Arg Ile Glu Thr Ile Leu Met Met Tyr Thr Arg Asn  
65 70 75 80  
Asn Leu Asn Cys Ala Glu Pro Leu Phe Glu Gln Asn Asn Ser Leu Asn  
85 90 95  
Val Asn Phe Asn Thr Gln Lys Lys Thr Val Trp Leu Ile His Gly Tyr  
100 105 110  
Arg Pro Val Gly Ser Ile Pro Leu Trp Leu Gln Asn Phe Val Arg Ile  
115 120 125  
Leu Leu Asn Glu Glu Asp Met Asn Val Ile Val Val Asp Trp Ser Arg  
130 135 140  
Gly Ala Thr Thr Phe Ile Tyr Asn Arg Ala Val Lys Asn Thr Arg Lys  
145 150 155 160  
Val Ala Val Ser Leu Ser Val His Ile Lys Asn Leu Leu Lys His Gly  
165 170 175  
Ala Ser Leu Asp Asn Phe His Phe Ile Gly Val Ser Leu Gly Ala His  
180 185 190  
Ile Ser Gly Phe Val Gly Lys Ile Phe His Gly Gln Leu Gly Arg Ile  
195 200 205  
Thr Gly Leu Asp Pro Ala Gly Pro Arg Phe Ser Arg Lys Pro Pro Tyr  
210 215 220  
Ser Arg Leu Asp Tyr Thr Asp Ala Lys Phe Val Asp Val Ile His Ser  
225 230 235 240  
Asp Ser Asn Gly Ile Gln Phe Ile Lys Cys Asn His Gln Arg Ala Val  
245 250 255  
His Leu Phe Met Ala Ser Leu Glu Thr Asn Cys Asn Phe Ile Ser Phe

260 265 270

Pro Cys Arg Ser Tyr Lys Asp Tyr Lys Thr Ser Leu Cys Val Asp Cys  
275 280 285

Asp Cys Phe Lys Glu Lys Ser Cys Pro Arg Leu Gly Tyr Gln Ala Lys  
290 295 300

Leu Phe Lys Gly Val Leu Lys Glu Arg Met Glu Gly Arg Pro Leu Arg  
305 310 315 320

Thr Thr Val Phe Leu Asp Thr Ser Ala Tyr Tyr Phe Val Leu Ser Ile  
325 330 335

Ile Val Pro Asp Lys Thr Met Met Asp Gly Ser Phe Ser Phe Lys Leu  
340 345 350

Leu Asn Gln Leu Gly Met Ile Glu Glu Pro Arg Leu Tyr Glu Glu Arg  
355 360 365

<210> 49  
<211> 1221  
<212> DNA  
<213> Homo sapiens

<400> 49  
ggaaaagctg agaataatca cctctgataa agatcacaga agctgcccgg gaggtgtttg 60  
attaaattca tgtattgaaa atattgttca gaccccatgt gacataactg gagccagtgc 120  
agtgccatga agaactacga gattagcctg gatattaact tgtcttctag agaatagatt 180  
tcatgtttca ttcttctgca atgggttaatt cacacagaaa accaatgttt aacattcaca 240  
gaggatttta ctgcttaaca gccatcttgc cccaaatatg catttggtct cagttctcag 300  
tgccatctag ttatcacttc actgaggatc ctggggcctt cccagtagcc actaatgggg 360  
aacgatttcc ttggcaggag ctaaggctcc ccagtgtggt cattcctctc cattatgacc 420  
tctttgtcca ccccaatctc acctctctgg actttgttgc atctgagaag atogaagtct 480  
tggtcagcaa tgctacccag tttatcatct tgcacagcaa agatcttgaa atcacgaatg 540  
ccacccttca gtcagaggaa gattcaagat acatgaaacc aggaaaagaa ctgaaagtgt 600  
tgagttaccc tgctcatgaa caaattgcac tgctggttcc agagaaactt acgcctcacc 660  
tgaaatacta tgtggctatg gacttccaag ccaagttagg tgatggcttt gaagggtttt 720  
ataaaagcac atacagaact cttggtggtg aaacaagaat tcttgcagta acagattttg 780  
agccaaccca ggcaagcatg gctttccctt gctttgatga accgttggtc aaagccaact 840  
tttcaatcaa gatacgaaga gagagcaggc atattgcact atccaacatg ccaaaggtgt 900  
ccatctatgc atccccagac aaacggaatc aaacacatta tgctttgcag gcatcactga 960  
agctacttga tttttatgaa aagtactttg atatctacta tccactctcc aaactgggta 1020  
tgttcaaatt ccacattatt gtcttcattt ttgctcataa aacttgctta gatctcttcc 1080  
ctctttctct ttgtatgtga tttaaatgag cactgaggaa ttcagtttagc tcaggaaaaa 1140  
ataatttggt cctcagagat gattcttgag tgtagaaaat aaaatattta tgacatgccc 1200  
caaaaaaaaa aaaaaaaaaa a 1221

<210> 50  
<211> 305  
<212> PRT  
<213> Homo sapiens

<400> 50  
Met Phe His Ser Ser Ala Met Val Asn Ser His Arg Lys Pro Met Phe  
1 5 10 15

Asn Ile His Arg Gly Phe Tyr Cys Leu Thr Ala Ile Leu Pro Gln Ile  
20 25 30

Cys Ile Cys Ser Gln Phe Ser Val Pro Ser Ser Tyr His Phe Thr Glu  
 35 40 45  
 Asp Pro Gly Ala Phe Pro Val Ala Thr Asn Gly Glu Arg Phe Pro Trp  
 50 55 60  
 Gln Glu Leu Arg Leu Pro Ser Val Val Ile Pro Leu His Tyr Asp Leu  
 65 70 75 80  
 Phe Val His Pro Asn Leu Thr Ser Leu Asp Phe Val Ala Ser Glu Lys  
 85 90 95  
 Ile Glu Val Leu Val Ser Asn Ala Thr Gln Phe Ile Ile Leu His Ser  
 100 105 110  
 Lys Asp Leu Glu Ile Thr Asn Ala Thr Leu Gln Ser Glu Glu Asp Ser  
 115 120 125  
 Arg Tyr Met Lys Pro Gly Lys Glu Leu Lys Val Leu Ser Tyr Pro Ala  
 130 135 140  
 His Glu Gln Ile Ala Leu Leu Val Pro Glu Lys Leu Thr Pro His Leu  
 145 150 155 160  
 Lys Tyr Tyr Val Ala Met Asp Phe Gln Ala Lys Leu Gly Asp Gly Phe  
 165 170 175  
 Glu Gly Phe Tyr Lys Ser Thr Tyr Arg Thr Leu Gly Gly Glu Thr Arg  
 180 185 190  
 Ile Leu Ala Val Thr Asp Phe Glu Pro Thr Gln Ala Arg Met Ala Phe  
 195 200 205  
 Pro Cys Phe Asp Glu Pro Leu Phe Lys Ala Asn Phe Ser Ile Lys Ile  
 210 215 220  
 Arg Arg Glu Ser Arg His Ile Ala Leu Ser Asn Met Pro Lys Val Ser  
 225 230 235 240  
 Ile Tyr Ala Ser Pro Asp Lys Arg Asn Gln Thr His Tyr Ala Leu Gln  
 245 250 255  
 Ala Ser Leu Lys Leu Leu Asp Phe Tyr Glu Lys Tyr Phe Asp Ile Tyr  
 260 265 270  
 Tyr Pro Leu Ser Lys Leu Gly Met Phe Lys Phe His Ile Ile Val Phe  
 275 280 285  
 Ile Phe Ala His Lys Thr Cys Leu Asp Leu Phe Pro Leu Ser Leu Cys  
 290 295 300  
 Met  
 305

<210> 51  
 <211> 951  
 <212> DNA  
 <213> Homo sapiens

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<400> 51
ggtgggtgcg gagtctgcgg ccgttcccgc ggctctctcc tcttccccgt tcccttcacc 60
cccccccgcc acccctttcc ccatcccggc tccgtcacc tcccgctccc cactcagg 120
acaagaatgc cctgcccgga acaaccagc agcgccctaga tggctttggt caggtccag 180
cggtcaccta ccccagcac cactccagc ccctgcgcct cggaggcaga cagtggggag 240
gaagaatgcc ggtcacagcc caggagcatc agcgagagct ttctaactgt caaaggtgct 300
gccctttttc taccacgggg aaatgggtca tccacaccaa gaatcagcca cagacggaac 360
aagcatgcag gcgatctcca acagcatctc caagcaatgt tcattttact ccgcccagaa 420
gacaacatca ggctggctgt aagactggaa agtacttacc agaatcgaa acgctatatg 480
gtagtgggtt caactaatgg tagacaagac actgaagaaa gcatcgctct aggaatggat 540
ttctctctta atgacagcac ttgtaccatg ggcttagttt tgcctctctg gagcgacacg 600
ctaattcatt tggatggtga tgggtgggttc agtgatcgga cggataacag agttcacata 660
ttcaaactcg tatctgtgca ggcaatgtgg gttgacaggg attcaaggaa caaactgt 720
gatgtactat tgggtggaaga atgaactgga gcagcctttc tggagagtga tttgccaata 780
tgccttatca ttttgcatga tctttgtcct agtaactcta tttctatgga tttactctaa 840
gtttgtaaac atggatgtgt gcaaagattt tagctctaag aatgtttgtc agtgttctaa 900
taatagcaaa aaataaaaaa caaatgattg aaaaaataaa aaaaaaaaaa a 951

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<210> 52
<211> 194
<212> PRT
<213> Homo sapiens

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<400> 52
Met Ala Leu Val Thr Val Gln Arg Ser Pro Thr Pro Ser Thr Thr Ser
  1              5              10              15

Ser Pro Cys Ala Ser Glu Ala Asp Ser Gly Glu Glu Glu Cys Arg Ser
      20              25              30

Gln Pro Arg Ser Ile Ser Glu Ser Phe Leu Thr Val Lys Gly Ala Ala
      35              40              45

Leu Phe Leu Pro Arg Gly Asn Gly Ser Ser Thr Pro Arg Ile Ser His
      50              55              60

Arg Arg Asn Lys His Ala Gly Asp Leu Gln Gln His Leu Gln Ala Met
      65              70              75              80

Phe Ile Leu Leu Arg Pro Glu Asp Asn Ile Arg Leu Ala Val Arg Leu
      85              90              95

Glu Ser Thr Tyr Gln Asn Arg Thr Arg Tyr Met Val Val Val Ser Thr
      100             105             110

Asn Gly Arg Gln Asp Thr Glu Glu Ser Ile Val Leu Gly Met Asp Phe
      115             120             125

Ser Ser Asn Asp Ser Thr Cys Thr Met Gly Leu Val Leu Pro Leu Trp
      130             135             140

Ser Asp Thr Leu Ile His Leu Asp Gly Asp Gly Gly Phe Ser Val Ser
      145             150             155             160

Thr Asp Asn Arg Val His Ile Phe Lys Pro Val Ser Val Gln Ala Met
      165             170             175

Trp Val Asp Arg Asp Ser Arg Asn Lys His Cys Asp Val Leu Leu Val
      180             185             190

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Glu Glu

<210> 53  
<211> 1514  
<212> DNA  
<213> Homo sapiens

<400> 53  
gcatgatatt tttacggttc acccatattg catgtatcag gaatataatc ctttttatta 60  
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gattttgggg ttttttcaca ttgcgctatt cagtataaac ctgctctcaa cattcatgtg 180  
caagtctttg agtggacata tatttgcgtt tctcttgagt gaatgcacct tgttgggtca 240  
cgtggcttaa cttaaaaaaa ttttaatcac tgtgggtgcat atgtagtgat tattagtgat 300  
tatctcataa ttttattttc ttgtttaatg atgttgagtg tatttcattt gtattttagt 360  
ttgcaaagt ttgttcaaat tcttcacctg tttttaatga agacgtacga cttatttttg 420  
tgttctgaac ataagttctt tgtcacataa aatgtgctat gaatgttgag ttttaaatac 480  
tccaaatgaa tggctagaga attactatct gtagaaatat ttatatgtca aagggatgct 540  
aacaatttac tttattgctc taaaaataga aagttgccag aatgctgtgg agtttttagtg 600  
gaaaacatga tagctggtgt tactgagtaa atttgagtgt taaatgtcaa tgtaagctaa 660  
cggccaagat agggaccact gcagggtggt tacttgacgc tgtgactcaa ctggtccttc 720  
actgccaaac atacctgggg ttggatcatt ggcctgacgt ttgcaaattg aggaacctta 780  
gggcaaataca gtgaacttct gaactgcctt cgtcttcagt tatatgggga tttcccccact 840  
tttgagatcc ttgtaaggat tatatgagat gaagagatga gacaaggat ataaaagtcc 900  
tagcacagag cgtgtcatat aatatggctt cacaagtacc ctcactctct ttcagtcgt 960  
tttttgtttt tgtttttgtt tttttgagac catctcactc tgttgcccag gctggagtgc 1020  
ctcttcattt ttatttcttt attcagcaag tattgatcaa atgtgctttg taccaggtac 1080  
tgagctcttc gttgggatat aatggtgatc aaggagattg tagattctgg cagggaatac 1140  
tgacatcaaa cacggcgacc cgacatagtg agacctgtc tctactagaa gaactttaaa 1200  
aatcacctag gtgtgggccc ggcacggtgg ctaacgcctg tgggccagc actttgggat 1260  
gctgaggcgg gtggatcacg gggtcaggag atcgagacca tcctggataa cacggagaaa 1320  
ccccgtctct actggaaata caaggaaatt ggccgggctg gggggcgggc atctgtggtc 1380  
ccaattactc gggaggctgc agcaggagag tggcatgaac ccgggaggcg gatcttgcac 1440  
tgagccgaga tcacgccact gcactccagc ctggggcgaca gaatgagact ccatctcaaa 1500  
aaaaaaaaaa aaaa 1514

<210> 54  
<211> 91  
<212> PRT  
<213> Homo sapiens

<400> 54  
Met Ala Ser Gln Val Pro Ser Ser Pro Phe Gln Ser Phe Phe Val Phe  
1 5 10 15  
Val Phe Val Phe Leu Arg Pro Ser His Ser Val Ala Gln Ala Gly Val  
20 25 30  
Pro Leu His Phe Tyr Phe Phe Ile Gln Gln Val Leu Ile Lys Cys Ala  
35 40 45  
Leu Tyr Gln Val Leu Ser Ser Ser Leu Gly Tyr Asn Gly Asp Gln Gly  
50 55 60  
Asp Cys Arg Phe Trp Gln Gly Lys Leu Thr Ser Asn Thr Ala Thr Arg  
65 70 75 80  
His Ser Glu Thr Leu Ser Leu Leu Glu Glu Leu

<210> 55  
 <211> 1417  
 <212> DNA  
 <213> Homo sapiens

<400> 55  
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 agcagtcaac caacatattt ctttcccaga gtcccatgaa taatcttcag actaacacag 180  
 tagcccaaga agcatttttt gcagcaccga actcaatttc tccacttcag tcaacatcaa 240  
 acagtgaaca acaagctgct ttccaacagc aagctccaat atcacacatc cagactccta 300  
 tgctttccca agaacaggca caacccccgc agcagggttt atttcagcct cagggtggcc 360  
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 agcactcaat agttgccatg cagagtaact ctccatccca ggaacagcag cagcagcagc 480  
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 <212> PRT  
 <213> Homo sapiens

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 35 40 45  
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 50 55 60  
 Ser Glu Gln Gln Ala Ala Phe Gln Gln Gln Ala Pro Ile Ser His Ile  
 65 70 75 80  
 Gln Thr Pro Met Leu Ser Gln Glu Gln Ala Gln Pro Pro Gln Gln Gly  
 85 90 95  
 Leu Phe Gln Pro Gln Val Ala Leu Gly Ser Leu Pro Pro Asn Pro Met  
 100 105 110



Pro Gln Ser Gln Gln Gly Thr Met Phe Gln Ser Gln His Ser Ile Val  
 115 120 125  
 Ala Met Gln Ser Asn Ser Pro Ser Gln Glu Gln Gln Gln Gln Gln  
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 145 150 155 160  
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 165 170 175  
 Asn Met Ile Phe Asn Pro Asn Gln Asn Pro Met Ala Asn Gln Glu Gln  
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 195 200 205  
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 225 230 235 240  
 Phe His Ser Ser Pro Gln Ile Gln Leu Val Gln Gly Ser Pro Ser Ser  
 245 250 255  
 Gln Glu Gln Gln Val Thr Leu Phe Leu Ser Pro Ala Ser Met Ser Ala  
 260 265 270  
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 Gln Pro Gln Ala Thr Leu Phe His Asn Thr Ala Gly Gly Thr Met Asn  
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 325 330 335  
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 <211> 2297  
 <212> DNA  
 <213> Homo sapiens

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<210> 58  
 <211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 58  
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Gly	Thr	Leu	Leu	Met	Lys	Arg	Lys	Phe	Glu	Glu	Pro	Arg	Pro	Gly	Phe	50	55	60	
His	Gly	Val	Leu	Gly	Ile	Asn	Ser	Ile	Thr	Gly	Lys	Glu	Glu	Pro	Leu	65	70	75	80
Tyr	Pro	Ser	Tyr	Lys	Arg	Gln	Leu	Arg	Ile	Tyr	Leu	Val	Ser	Leu	Pro	85	90	95	
Phe	Val	Cys	Leu	Cys	Leu	Tyr	Phe	Ser	Leu	Tyr	Val	Met	Met	Ile	Tyr	100	105	110	
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Val	Ile	Glu	Ile	Met	Asn	Arg	Leu	Tyr	Arg	Tyr	Ala	Ala	Glu	Phe	Leu	145	150	155	160
Thr	Ser	Trp	Glu	Asn	His	Arg	Leu	Glu	Ser	Ala	Tyr	Gln	Asn	His	Leu	165	170	175	
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Cys	Val	Tyr	Pro	Leu	Ala	Ala	Ala	Phe	Ala	Val	Leu	Asn	Asn	Phe	Thr	290	295	300	
Glu	Val	Asn	Ser	Asp	Ala	Leu	Lys	Met	Cys	Arg	Val	Phe	Lys	Arg	Pro	305	310	315	320
Phe	Ser	Glu	Pro	Ser	Ala	Asn	Ile	Gly	Val	Trp	Gln	Met	Ile	Phe	Cys	325	330	335	
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 370 375

<210> 59  
 <211> 4145  
 <212> DNA  
 <213> Homo sapiens

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 <213> Homo sapiens

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 35 40 45  
 Asn Ile Gln Val Ser His Gln Glu Phe Ser Lys Met Lys Gln Ser Asn  
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 65 70 75 80  
 Tyr Asp Asn Phe Val Glu Leu Val Ala Asn Leu Lys Glu Gly Thr Lys  
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 Ser Asp Ile Val Phe Ala Arg Lys Thr Glu Arg Asp Glu Leu Leu Lys  
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 Asp Leu Gln Gln Ser Ile Ala Arg Glu Pro Ser Ala Pro Ser Ile Pro  
 130 135 140  
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Pro Thr Pro Ala Pro Arg Thr Met Pro Pro Thr Lys Pro Gln Pro Pro  
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Ala Arg Pro Pro Pro Pro Val Leu Pro Ala Asn Arg Ala Pro Ser Ala  
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Thr Ala Pro Ser Pro Val Gly Ala Gly Thr Ala Ala Pro Ala Pro Ser  
195 200 205

Gln Thr Pro Gly Ser Ala Pro Pro Pro Gln Ala Gln Gly Pro Pro Tyr  
210 215 220

Pro Thr Tyr Pro Gly Tyr Pro Gly Tyr Cys Gln Met Pro Met Pro Met  
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Gly Tyr Asn Pro Tyr Ala Tyr Gly Gln Tyr Asn Met Pro Tyr Pro Pro  
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Pro Ser Tyr Pro Phe Pro Gln Pro Pro Gln Gln Ser Tyr Tyr Pro Gln  
275 280 285

Gln

<210> 61  
<211> 1417  
<212> DNA  
<213> Homo sapiens

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<210> 62

<211> 414  
 <212> PRT  
 <213> Homo sapiens

<400> 62

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Phe Ser Ala Ala Ala Leu Ile Pro Thr Gly Asp Gly Gln Asn Leu Phe
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Thr Lys Asp Val Thr Val Ile Glu Gly Glu Val Ala Thr Ile Ser Cys
  50              55              60

Gln Val Asn Lys Ser Asp Asp Ser Val Ile Gln Leu Leu Asn Pro Asn
  65              70              75              80

Arg Gln Thr Ile Tyr Phe Arg Asp Phe Arg Pro Leu Lys Asp Ser Arg
  85              90              95

Phe Gln Leu Leu Asn Phe Ser Ser Ser Glu Leu Lys Val Ser Leu Thr
  100             105             110

Asn Val Ser Ile Ser Asp Glu Gly Arg Tyr Phe Cys Gln Leu Tyr Thr
  115             120             125

Asp Pro Pro Gln Glu Ser Tyr Thr Thr Ile Thr Val Leu Val Pro Pro
  130             135             140

Arg Asn Leu Met Ile Asp Ile Gln Lys Asp Thr Ala Val Glu Gly Glu
  145             150             155             160

Glu Ile Glu Val Asn Cys Thr Ala Met Ala Ser Lys Pro Ala Thr Thr
  165             170             175

Ile Arg Trp Phe Lys Gly Asn Thr Glu Leu Lys Gly Lys Ser Glu Val
  180             185             190

Glu Glu Trp Ser Asp Met Tyr Thr Val Thr Ser Gln Leu Met Leu Lys
  195             200             205

Val His Lys Glu Asp Asp Gly Val Pro Val Ile Cys Gln Val Glu His
  210             215             220

Pro Ala Val Thr Gly Asn Leu Gln Thr Gln Arg Tyr Leu Glu Val Gln
  225             230             235             240

Tyr Lys Pro Gln Val His Ile Gln Met Thr Tyr Pro Leu Gln Gly Leu
  245             250             255

Thr Arg Glu Gly Asp Ala Leu Glu Leu Thr Cys Glu Ala Ile Gly Lys
  260             265             270

Pro Gln Pro Val Met Val Thr Trp Val Arg Val Asp Asp Glu Met Pro
  275             280             285

Gln His Ala Val Leu Ser Gly Pro Asn Leu Phe Ile Asn Asn Leu Asn

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290                      295                      300  
 Lys Thr Asp Asn Gly Thr Tyr Arg Cys Glu Ala Ser Asn Ile Val Gly  
 305                      310                      315                      320  
 Lys Ala His Ser Asp Tyr Met Leu Tyr Val Tyr Asp Ser Arg Ala Gly  
                      325                      330                      335  
 Glu Glu Gly Ser Ile Arg Ala Val Asp His Ala Val Ile Gly Gly Val  
                      340                      345                      350  
 Val Ala Val Val Val Phe Ala Met Leu Cys Leu Leu Ile Ile Leu Gly  
                      355                      360                      365  
 Arg Tyr Phe Ala Arg His Lys Gly Thr Tyr Phe Thr His Glu Ala Lys  
                      370                      375                      380  
 Gly Ala Asp Asp Ala Ala Asp Ala Asp Thr Ala Ile Ile Asn Ala Glu  
 385                      390                      395                      400  
 Gly Gly Gln Asn Asn Ser Glu Glu Lys Lys Glu Tyr Phe Ile  
                      405                      410

<210> 63  
 <211> 1571  
 <212> DNA  
 <213> Homo sapiens

<400> 63  
 ggccgcggag actgcgaccc tcttctctca gtctgcctta ctaccatgcc gctctacgag 60  
 ggccctgggga gcggcgggga gaagacggcg gtcgtgatcg acctgggaga ggcctttacc 120  
 aagtgtggat ttgctggaga aactgggtcca agatgtataa ttcttagtgt gataaaaaga 180  
 gctgggatgc ctaagcctgt cagagttgtt cagtataata tcaatacaga agaattatat 240  
 tctacctaag aggaattcat ccacatacta tatttcaggc atctatttgt gaatcccaga 300  
 gaccgcggag ttgtgattat cgaatcggta ttatgtcctt ctcaacttcag agagacactc 360  
 actcgtgttc ttttcaaata ttttgaggtt ccatctgtct tgcttgctcc aagtcactca 420  
 atggctcttc tgacgcttgg aattaattct gccatgggtc tagatttgtg atatagggaa 480  
 agcctgggtg taccatata tgaaggaaat ccagttctaa attgttggg agcactaccc 540  
 ctaggaggaa aagctcttca caaagagttg gaaactcaac tattggaaca atgtactgtt 600  
 gacacaagtg ttgctaaaga acagagcctt ccctcagtga tgggttcagt tccggaaggt 660  
 gtcttagagg acattaaagc gcgtacttgc tttgtaagt atctgaagcg aggactaaaa 720  
 atccaagcag caaaatttaa tattgatggg aataatgagc gtccctcccc acccccaa 780  
 gttgactatc cattagatgg agagaagatt ttacatatcc ttggatcaat cagagattca 840  
 gttgtggaat ttctttttga acaagataat gaagagcaat cagttgccac tttaatattg 900  
 gattccctta tacagtgtcc gatagacacc aggaagcaac tagcagagaa tttggtagtc 960  
 atagggtggc cttctatgtt gccaggattt ctccacagat tgcttgacaga aataaggtat 1020  
 ttggtagaaa aacccaaaata taaaaaagca cttggcacta agacatttcg aattcatact 1080  
 ccacctgcaa aagctaattg tgtggcctgg ttgggagggg ctattttttg agcattacaa 1140  
 gatatacttg ggagccgttc tgtttcaaag gaattattata atcagacggg ccgtatacct 1200  
 gattggtgtt ctctcaataa ccacaccttg gaaatgatgt ttgatgtcgg gaaaactcaa 1260  
 ccacctctga tgaagagagc attttccact gagaaataga agtttgatta aaaatcaacc 1320  
 ttgcttcata tcaaatattt aaccaattat aagcaaatg taaaaagat gtaggatgtt 1380  
 ttgttataga ggactatagt ggaagtgaat gcattctgtg tttactcttt gcattaatat 1440  
 ataattcttt tgactttgtt tctcttgtgt agtggtaaaa tggtagctgg tgcttattga 1500  
 gatttgcgtg atttatatca ataaagtata gtaaagcaaa aaaaaaaaaa aaaaaaaaaa 1560  
 aaaaaaaaaa a 1571

<210> 64  
 <211> 417



<212> PRT

<213> Homo sapiens

<400> 64

Met Pro Leu Tyr Glu Gly Leu Gly Ser Gly Gly Glu Lys Thr Ala Val  
1 5 10 15

Val Ile Asp Leu Gly Glu Ala Phe Thr Lys Cys Gly Phe Ala Gly Glu  
20 25 30

Thr Gly Pro Arg Cys Ile Ile Pro Ser Val Ile Lys Arg Ala Gly Met  
35 40 45

Pro Lys Pro Val Arg Val Val Gln Tyr Asn Ile Asn Thr Glu Glu Leu  
50 55 60

Tyr Ser Tyr Leu Lys Glu Phe Ile His Ile Leu Tyr Phe Arg His Leu  
65 70 75 80

Leu Val Asn Pro Arg Asp Arg Arg Val Val Ile Ile Glu Ser Val Leu  
85 90 95

Cys Pro Ser His Phe Arg Glu Thr Leu Thr Arg Val Leu Phe Lys Tyr  
100 105 110

Phe Glu Val Pro Ser Val Leu Leu Ala Pro Ser His Leu Met Ala Leu  
115 120 125

Leu Thr Leu Gly Ile Asn Ser Ala Met Val Leu Asp Cys Gly Tyr Arg  
130 135 140

Glu Ser Leu Val Leu Pro Ile Tyr Glu Gly Ile Pro Val Leu Asn Cys  
145 150 155 160

Trp Gly Ala Leu Pro Leu Gly Gly Lys Ala Leu His Lys Glu Leu Glu  
165 170 175

Thr Gln Leu Leu Glu Gln Cys Thr Val Asp Thr Ser Val Ala Lys Glu  
180 185 190

Gln Ser Leu Pro Ser Val Met Gly Ser Val Pro Glu Gly Val Leu Glu  
195 200 205

Asp Ile Lys Ala Arg Thr Cys Phe Val Ser Asp Leu Lys Arg Gly Leu  
210 215 220

Lys Ile Gln Ala Ala Lys Phe Asn Ile Asp Gly Asn Asn Glu Arg Pro  
225 230 235 240

Ser Pro Pro Pro Asn Val Asp Tyr Pro Leu Asp Gly Glu Lys Ile Leu  
245 250 255

His Ile Leu Gly Ser Ile Arg Asp Ser Val Val Glu Ile Leu Phe Glu  
260 265 270

Gln Asp Asn Glu Glu Gln Ser Val Ala Thr Leu Ile Leu Asp Ser Leu  
275 280 285

Ile Gln Cys Pro Ile Asp Thr Arg Lys Gln Leu Ala Glu Asn Leu Val  
290 295 300

Val Ile Gly Gly Thr Ser Met Leu Pro Gly Phe Leu His Arg Leu Leu  
 305 310 315 320

Ala Glu Ile Arg Tyr Leu Val Glu Lys Pro Lys Tyr Lys Lys Ala Leu  
 325 330 335

Gly Thr Lys Thr Phe Arg Ile His Thr Pro Pro Ala Lys Ala Asn Cys  
 340 345 350

Val Ala Trp Leu Gly Gly Ala Ile Phe Gly Ala Leu Gln Asp Ile Leu  
 355 360 365

Gly Ser Arg Ser Val Ser Lys Glu Tyr Tyr Asn Gln Thr Gly Arg Ile  
 370 375 380

Pro Asp Trp Cys Ser Leu Asn Asn Pro Pro Leu Glu Met Met Phe Asp  
 385 390 395 400

Val Gly Lys Thr Gln Pro Pro Leu Met Lys Arg Ala Phe Ser Thr Glu  
 405 410 415

Lys

<210> 65  
 <211> 1752  
 <212> DNA  
 <213> Homo sapiens

<400> 65  
 ggccaatcag agggacggcc ccagaatggc atggtagatg gaacgcagct gagaggctctg 60  
 acaagatgta ccagggtccca ctaccactgg atcggtatgg gacctggta cggctccgct 120  
 tcaccatggg ggccttggtc acggtctgct gtccacttgt cgccttccctc ttctgcatcc 180  
 tctgggtccct gctcttccac ttcaaggaga caacggccac acactgtggg gtgccaatt 240  
 acctgcccctc ggtgagctca gccatcggcg gggaggtgcc ccagcgctac gtgtggcggt 300  
 tctgcatcgg cctgcaactg gcgcctcgct tcttggtggc cttcgccctac tggaaccact 360  
 acctcagctg cacctccccg tgttctgctc atcgcccgct ctgcgcctc aacttcggcc 420  
 tcaatgtcgt ggagaacctc gcgttgetag tgetcaacta tgtctctcc tccgaggact 480  
 tcaccatcca cgaaaatgct ttcatgtgtg tcattgcctc atccctcggg cacatgctcc 540  
 tcacctgcat tctctggcgg ttgaccaaga agcacacagt aagtccaggag gatcgcaagt 600  
 cctacagctg gaaacagcgg ctcttcatca tcaacttcat ctctctcttc tcggcgctgg 660  
 ctgtctactt tcggcacaac atgtattgtg aggetggagt gtacaccatc tttgccatcc 720  
 tggagtacac tgttgtctta accaactatg cgttccacat gacggcctgg tgggacttcg 780  
 ggaacaagga gctgtcata acctctcagc ctgaggaaaa gcgattctga accttcagt 840  
 cctgcttggtg aggcgcgagc ccactgcccc gaaacaagaa acacgatacc attctggcct 900  
 tccccacccc acatctcttc ttggccttac tgaagatggg ggaagggtaa gaaggaaggg 960  
 tgtaggccaa ggctcaccct agtgctgctg gcttctctc tccaccctc atatgggctg 1020  
 ggggtcctca aacatcacct ttacctgaga ggccccaa gaagctgagctg gcagagagct 1080  
 ccaccatttg gtgctaaaaa aaaaaacgtc ctgaggttca tgaccaccat ccagtttctg 1140  
 gcctttacac agtcaccttt cactgaggtc aggagccct gagcagtggc tgctcctga 1200  
 caaccacagc catttctctg cacgggggtc attcatagga ctaatgtatt tcatgatcta 1260  
 ctgtgcacat ccaggcctgt ggccacagtc cctgctaaa gttgctcagg tgttctagtc 1320  
 ctgacttcac ctttttgatt tgggtgtgtg cctagggtat gtacccttc ccatctgagc 1380  
 ctcggtgtgt ccatgtgtct ggccggggat ggggtggactg tatgatttc aaggactcta 1440  
 ccagtacgtg gttctgatgt catcgggtgg aggtggtgtt ctatacctaa aggatgacct 1500  
 gctccagaaa cagcaccagc acagcatgta ttttctctc ttctgaaagt tctggcttgt 1560  
 agaccctcc cctcctttgc aaagggtatg gatagagggg tcagatgcag atctctactg 1620  
 taaaatgggc tccttggtat ctctgtctt ccctactgct ccaaacccta aattttggtt 1680



<212> DNA  
 <213> Homo sapiens

<400> 67  
 cactcctgca gacaaggcac tgattgcccc agaccatgta gttccagctc cagaagagtg 60  
 ctatgtgtat agtccattgg gctctgctta taaacttcaa agttacactg aaggatacgg 120  
 taaaaacacc agtttagtaa ccatttttat gatttggaaat accatgatgg gaacatctat 180  
 actaagcatt ccttggggca taaaacaggc tggatttact actggaatgt gtgtcatcat 240  
 actgatgggc cttttaacac tttattgctg ctacagagta gtgaaatcac ggactatgat 300  
 gttttcattg gataccacta cctgggaata tccagatgtc tgcagacatt atttcggctc 360  
 ctttgggcag tggtcgagtc tcctcttctc cttggtgtct ctcatgggag caatgatagt 420  
 ttattgggtg cttatgtcaa attttctttt taatactgga aagtttattt ttagtaagta 480  
 tctatatcat atgcttttaa cacagtactt tcaaatacta ttaccactgt aatgttagtt 540  
 ctagccttaa attctaggac ttgggataaa taaaataaga agtaacatat ataattttgg 600  
 aaaatatatt ttattcagtt ggctttctgt ggttgtgctc tcaaatatag tgtatgctta 660  
 tttccaaaca ttaatctttg aaggaataat attcctccaa aatccttagt taaaataaaa 720  
 tatgtctata atccaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 780  
 a 781

<210> 68  
 <211> 127  
 <212> PRT  
 <213> Homo sapiens

<400> 68  
 Met Ile Trp Asn Thr Met Met Gly Thr Ser Ile Leu Ser Ile Pro Trp  
 1 5 10 15  
 Gly Ile Lys Gln Ala Gly Phe Thr Thr Gly Met Cys Val Ile Ile Leu  
 20 25 30  
 Met Gly Leu Leu Thr Leu Tyr Cys Cys Tyr Arg Val Val Lys Ser Arg  
 35 40 45  
 Thr Met Met Phe Ser Leu Asp Thr Thr Thr Trp Glu Tyr Pro Asp Val  
 50 55 60  
 Cys Arg His Tyr Phe Gly Ser Phe Gly Gln Trp Ser Ser Leu Leu Phe  
 65 70 75 80  
 Ser Leu Val Ser Leu Ile Gly Ala Met Ile Val Tyr Trp Val Leu Met  
 85 90 95  
 Ser Asn Phe Leu Phe Asn Thr Gly Lys Phe Ile Phe Ser Lys Tyr Leu  
 100 105 110  
 Tyr His Met Leu Leu Thr Gln Tyr Phe Gln Ile Leu Leu Pro Leu  
 115 120 125

<210> 69  
 <211> 649  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 gagcaactcc cttccccatc tctgtctacc atgtggacgc tgaaatcgtc cctggctctg 60  
 cttctgtgcc tcacctgcag ctatgccttt atgttctctt ctctgagaca gaaaactagc 120  
 gaaccccagg ggaaggtgca atacggagag cactttcggg ttcggcagaa tctaccagag 180  
 cacacccaag gctggcttgg gagcaaatgg ctctggcttc tttttgttgt tgtgccgttt 240

gtgatactgc agtgtcaaag agacagtgcg aagaataagg agcagagtcc tcctggcctt 300  
cgaggcggcc aacttcactc tccattaaaag aaaaaaagaa atgcttcccc caacaaagac 360  
tgtgcattca ataccttaat ggaactcgag gtggagctta tgaaatttgt gtccaaagtg 420  
cggaatctta aacgtgccat ggcaacaggt agtggcagta acctcaggct tcgaaagtca 480  
gagatgcctg cagatccata ccatgtcacg atctgtgaaa tatggggaga agaaagctct 540  
agctgaatgg atttgtgtgt caggagagaa aaaagttgag tgttgacaaa ctgtatgcaa 600  
actaataaaa ctattctgaa gaaaagaaaa aaaaaaaaaa aaaaaaaaaa 649

<210> 70  
<211> 171  
<212> PRT  
<213> Homo sapiens

<400> 70  
Met Trp Thr Leu Lys Ser Ser Leu Val Leu Leu Cys Leu Thr Cys  
1 5 10 15  
Ser Tyr Ala Phe Met Phe Ser Ser Leu Arg Gln Lys Thr Ser Glu Pro  
20 25 30  
Gln Gly Lys Val Gln Tyr Gly Glu His Phe Arg Ile Arg Gln Asn Leu  
35 40 45  
Pro Glu His Thr Gln Gly Trp Leu Gly Ser Lys Trp Leu Trp Leu Leu  
50 55 60  
Phe Val Val Val Pro Phe Val Ile Leu Gln Cys Gln Arg Asp Ser Glu  
65 70 75 80  
Lys Asn Lys Glu Gln Ser Pro Pro Gly Leu Arg Gly Gly Gln Leu His  
85 90 95  
Ser Pro Leu Lys Lys Lys Arg Asn Ala Ser Pro Asn Lys Asp Cys Ala  
100 105 110  
Phe Asn Thr Leu Met Glu Leu Glu Val Glu Leu Met Lys Phe Val Ser  
115 120 125  
Lys Val Arg Asn Leu Lys Arg Ala Met Ala Thr Gly Ser Gly Ser Asn  
130 135 140  
Leu Arg Leu Arg Lys Ser Glu Met Pro Ala Asp Pro Tyr His Val Thr  
145 150 155 160  
Ile Cys Glu Ile Trp Gly Glu Glu Ser Ser Ser  
165 170

<210> 71  
<211> 1456  
<212> DNA  
<213> Homo sapiens

<400> 71  
cacggctgtc ttatctgcaa gtgcagagag gcctctgctt cagctggggc acccatcctg 60  
tcgggcactt gtctcaccgt ggatgggtcat catcataaaa atgaggagag ctggcaccgat 120  
gggtgccggg aatgctactg tctcaatgga cgggaaatgt gtgccctgat cacctgcccg 180  
gtgcctgcct gtggcaaccc caccattcac cctggacagt gctgcccac atgtgcagat 240  
gactttgtgg tgcagaagcc agagctcagt actccctcca ttgcccacgc ccttgaggga 300  
gaatactttg tggaaggaga aacgtggaac attgactcct gtactcagtg cacctgccac 360

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agcggacggg tgctgtgtga gacagaggtg tgcccaccgc tgctctgcca gaacccctca 420
cgcaaccagg attcctgctg cccacagtggt acagatcaac cttttcggcc ttccttgtcc 480
cgcaataaca gcgtacctaa ttattgcaaa aatgatgaag gggatatatt cctggcagct 540
gagtcctgga agcctgacgt ttgtaccagc tgcattctgca ttgatagcgt aattagctgt 600
ttctctgagt cctgcccctc tgtatcctgt gaaagacctg tcttgagaaa aggccagtgt 660
tgtccctact gcatagaaga cacaattcca aagaaggtgg tgtgccactt cagtgggaag 720
gcctatgccg acgaggagcg gtgggacctt gacagctgca cccactgcta ctgcctgcag 780
ggccagaccc tctgctcgac cgtcagctgc cccctctgct cctgtgttga gcccatcaac 840
gtggaaggaa gttgtgtccc aatgtgtcca gaaatgtatg tcccagaacc aaccaatata 900
cccattgaga agacaaacca tgcaggagag gttgacctgg aggttcccct gtggcccacg 960
cctagtgaia atgatatcgt ccattctcct agagatatgg gtcacctcca ggtagattac 1020
agagataaca ggctgcaccc aagtgaagat tcttcactgg actccattgc ctgagtgtg 1080
gttcccataa ttatatgcct ctctattata atagcattcc tattcatcaa tcagaagaaa 1140
cagtggatac cactgctttg ctggtatcga acaccaacta agccttcttc cttaataaat 1200
cagctagtat ctgtggactg caagaaagga accagagtcc aggtggacag tcccagaga 1260
atgctaagaa ttgcagaacc agatgcaaga ttcagtggct tctacagcat gcaaaaacag 1320
aaccatctac aggcagacaa tttctaccaa acagtgtgaa gaaaggcaac taggatgagg 1380
tttcaaaaga cggaagacga ctaaatctgc tctaaaaagt aaactagaat ttgtgcactt 1440
aaaaaaaaaa aaaaaa                                     1456

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<210> 72
<211> 400
<212> PRT
<213> Homo sapiens

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<400> 72
Met Cys Ala Leu Ile Thr Cys Pro Val Pro Ala Cys Gly Asn Pro Thr
  1                      5                      10                      15

Ile His Pro Gly Gln Cys Cys Pro Ser Cys Ala Asp Asp Phe Val Val
                20                      25                      30

Gln Lys Pro Glu Leu Ser Thr Pro Ser Ile Cys His Ala Pro Gly Gly
    35                      40                      45

Glu Tyr Phe Val Glu Gly Glu Thr Trp Asn Ile Asp Ser Cys Thr Gln
    50                      55                      60

Cys Thr Cys His Ser Gly Arg Val Leu Cys Glu Thr Glu Val Cys Pro
    65                      70                      75                      80

Pro Leu Leu Cys Gln Asn Pro Ser Arg Thr Gln Asp Ser Cys Cys Pro
                85                      90                      95

Gln Cys Thr Asp Gln Pro Phe Arg Pro Ser Leu Ser Arg Asn Asn Ser
    100                      105                      110

Val Pro Asn Tyr Cys Lys Asn Asp Glu Gly Asp Ile Phe Leu Ala Ala
    115                      120                      125

Glu Ser Trp Lys Pro Asp Val Cys Thr Ser Cys Ile Cys Ile Asp Ser
    130                      135                      140

Val Ile Ser Cys Phe Ser Glu Ser Cys Pro Ser Val Ser Cys Glu Arg
    145                      150                      155                      160

Pro Val Leu Arg Lys Gly Gln Cys Cys Pro Tyr Cys Ile Glu Asp Thr
                165                      170                      175

Ile Pro Lys Lys Val Val Cys His Phe Ser Gly Lys Ala Tyr Ala Asp

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180	185	190
Glu Glu Arg Trp Asp Leu Asp Ser Cys Thr His Cys Tyr Cys Leu Gln		
195	200	205
Gly Gln Thr Leu Cys Ser Thr Val Ser Cys Pro Pro Leu Pro Cys Val		
210	215	220
Glu Pro Ile Asn Val Glu Gly Ser Cys Cys Pro Met Cys Pro Glu Met		
225	230	235
Tyr Val Pro Glu Pro Thr Asn Ile Pro Ile Glu Lys Thr Asn His Arg		
245	250	255
Gly Glu Val Asp Leu Glu Val Pro Leu Trp Pro Thr Pro Ser Glu Asn		
260	265	270
Asp Ile Val His Leu Pro Arg Asp Met Gly His Leu Gln Val Asp Tyr		
275	280	285
Arg Asp Asn Arg Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile		
290	295	300
Ala Ser Val Val Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala		
305	310	315
Phe Leu Phe Ile Asn Gln Lys Lys Gln Trp Ile Pro Leu Leu Cys Trp		
325	330	335
Tyr Arg Thr Pro Thr Lys Pro Ser Ser Leu Asn Asn Gln Leu Val Ser		
340	345	350
Val Asp Cys Lys Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg		
355	360	365
Met Leu Arg Ile Ala Glu Pro Asp Ala Arg Phe Ser Gly Phe Tyr Ser		
370	375	380
Met Gln Lys Gln Asn His Leu Gln Ala Asp Asn Phe Tyr Gln Thr Val		
385	390	395
		400

<210> 73  
 <211> 4723  
 <212> DNA  
 <213> Homo sapiens

<400> 73  
 ggccttcatg gcctatTTTT tttttttttt aaatgataca acttaatttt attaggacaa 60  
 ggctgggtggg cactggagtg gcaccttcag ggccaggaga ggcaactgggg aggggtcaca 120  
 ggatgctact cgggcaccta gaagccacag ctgccctcca cagagcggca ctgcaccatg 180  
 cgcaggaatg tctcgacctt gtccatgtcc ttcttgaagc agtagagcag cccgtagttc 240  
 ttgagcagtg cgctcatggtt gtgcgagttt gtgtcaaact tgctgtaggt ctgcttgagg 300  
 atctgcccag tccggcggct gccgtcttcc agcctcccca tcagcgtttg gatgccttcc 360  
 tctaggtcct ttagggagtg atagtcatcg ttgtccgagg tgtcatacac cagggtgttg 420  
 gcgaacatac tcctgaggaa cgcacgggc tccagccacg actcgatgag cagcagggag 480  
 atgcgagca gctctagatt ggatttctgt tgcgtttcct ccatgttgga ggggtgtcga 540  
 atagagtctg agaagcagaa ggaggtcttg gagtcatgca ggaatgaata cttctgggtcc 600  
 tttgggatat aggtttcttc aaactcctgg taggtgtcaa tggccagctg gtgcgcgcga 660  
 tgggcttgga gcatagcgtg gtcaaaaagc ctggataacg gaacggtttg gacggcacca 720

gcctcttgaa	gccagggcag	gcagagcagg	gcaaaagcca	ggagcaggga	cytcocgggag	780
ctctggagcca	ttgccactag	gtgagctgtc	cacagagacc	tgagtggttc	ggggagttcg	840
gccttcatgg	cctaggagcg	ggcgaggagt	gaggcgagcg	gggcgcgcgg	agcggacgcc	900
gcg gatcttg	tgctgcgcca	cgcgcgccac	tcggcagctc	gggagcgggg	gaccggccccg	960
gaggctgcgc	cgctgcgggg	cgggccgact	cggagaggga	gagggaggag	gcgccgcgcg	1020
ccggggctgg	agccgagcgc	agcagccacc	gccgcgcgcg	cgccagaagt	ttgggttgaa	1080
ccggagctgc	cgggaggaaa	cttttttctt	ttttccccc	ccctccccgg	aggaggaggga	1140
ggaggaggag	gggaagctgc	cgcgcgcgc	aaggctcgtg	ggctcgggg	cgcgcgcgcc	1200
cgcagaagg	gcgggggcct	gcgcccgca	ggggagcgcg	gccccgggg	ccccgagagg	1260
cccggtgagg	acgcggggct	gctggtgcgg	cggcggcggc	ggcgcggtg	ccccgcgcag	1320
gggagggcgc	ccgccccgct	cccgccccgg	ctgcgaggag	gaggcgcgcg	cggcgcaggga	1380
ggatgtactt	ggtggcgggg	gacaggggg	tggccggctg	cgggcacctc	ctggtctcgc	1440
tgctggggct	gctgctgctg	ctggcgcgct	ccggcacccg	ggcgctgggt	tgcttgcctt	1500
gtgacgagtc	caagtgcgag	gagcccagga	actgcccggg	gagcatcgtg	cagggcgctt	1560
gcggctgctg	ctacacgtgc	gccagccaga	ggaagcagag	ctgcggcgcc	accttcggga	1620
tttcggaac	ctgcgacggc	gggctgcgtt	gtgtcatccg	cccccgctc	aatggcgact	1680
cctcaccca	gtacgaagcg	ggcgtttgcy	aagatgagaa	ctggactgat	gaccaactgc	1740
ttggttttaa	accatgcaat	gaaaacctta	ttgctggctg	caatataatc	aatgggaaat	1800
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<212> PRT
<213> Homo sapiens

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Arg Ala Leu Val Cys Leu Pro Cys Asp Glu Ser Lys Cys Glu Glu Pro
      35             40             45

Arg Asn Cys Pro Gly Ser Ile Val Gln Gly Val Cys Gly Cys Cys Tyr
      50             55             60

Thr Cys Ala Ser Gln Arg Asn Glu Ser Cys Gly Gly Thr Phe Gly Ile
      65             70             75             80

Tyr Gly Thr Cys Asp Arg Gly Leu Arg Cys Val Ile Arg Pro Pro Leu
      85             90             95

Asn Gly Asp Ser Leu Thr Glu Tyr Glu Ala Gly Val Cys Glu Asp Glu
      100            105            110

Asn Trp Thr Asp Asp Gln Leu Leu Gly Phe Lys Pro Cys Asn Glu Asn
      115            120            125

Leu Ile Ala Gly Cys Asn Ile Ile Asn Gly Lys Cys Glu Cys Asn Thr
      130            135            140

Ile Arg Thr Cys Ser Asn Pro Phe Glu Phe Pro Ser Gln Asp Met Cys
      145            150            155            160

Leu Ser Ala Leu Lys Arg Ile Glu Glu Glu Lys Pro Asp Cys Ser Lys
      165            170            175

Ala Arg Cys Glu Val Gln Phe Ser Pro Arg Cys Pro Glu Asp Ser Val
      180            185            190

Leu Ile Glu Gly Tyr Ala Pro Pro Gly Glu Cys Cys Pro Leu Pro Ser
      195            200            205

Arg Cys Val Cys Asn Pro Ala Gly Cys Leu Arg Lys Val Cys Gln Pro
      210            215            220

Gly Asn Leu Asn Ile Leu Val Ser Lys Ala Ser Gly Lys Pro Gly Glu
      225            230            235            240

Cys Cys Asp Leu Tyr Glu Cys Lys Pro Val Phe Gly Val Asp Cys Arg

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 Leu His Pro Ser Glu Asp Ser Ser Leu Asp Ser Ile Ala Ser Val Val  
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 Val Pro Ile Ile Ile Cys Leu Ser Ile Ile Ile Ala Phe Leu Phe Ile  
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 Lys Gly Thr Arg Val Gln Val Asp Ser Ser Gln Arg Met Leu Arg Ile  
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 Arg Trp His Pro Tyr Leu Glu Pro Tyr Gly Leu Val Tyr Cys Val Asn  
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Cys Ile Cys Ser Glu Asn Gly Asn Val Leu Cys Ser Arg Val Arg Cys  
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 Pro Asn Val His Cys Leu Ser Pro Val His Ile Pro His Leu Cys Cys  
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 Pro Arg Cys Pro Asp Ser Leu Pro Pro Val Asn Asn Lys Val Thr Ser  
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 Lys Ser Cys Glu Tyr Asn Gly Thr Thr Tyr Gln His Gly Glu Leu Phe  
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 Val Ala Glu Gly Leu Phe Gln Asn Arg Gln Pro Asn Gln Cys Thr Gln  
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 Val Cys Arg Gly Asp Gly Glu Leu Ser Trp Glu His Ser Asp Gly Asp  
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 Ser His Tyr Asp Pro Pro Pro Ser Arg Gln Ala Gly Gly Leu Ser Arg  
 210 215 220  
 Phe Pro Gly Ala Arg Ser His Arg Gly Ala Leu Met Asp Ser Gln Gln  
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 Ala Ser Gly Thr Ile Val Gln Ile Val Ile Asn Asn Lys His Lys His  
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 Gly Gln Val Cys Val Ser Asn Gly Lys Thr Tyr Ser His Gly Glu Ser  
 260 265 270  
 Trp His Pro Asn Leu Arg Ala Phe Gly Ile Val Glu Cys Val Leu Cys  
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 Arg Tyr Pro Cys Lys Tyr Pro Gln Lys Ile Asp Gly Lys Cys Cys Lys  
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 Val Cys Pro Gly Lys Lys Ala Lys Glu Glu Leu Pro Gly Gln Ser Phe  
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 Asp Asn Lys Gly Tyr Phe Cys Gly Glu Glu Thr Met Pro Val Tyr Glu  
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 Ser Val Phe Met Glu Asp Gly Glu Thr Thr Arg Lys Ile Ala Leu Glu  
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 Thr Glu Arg Pro Pro Gln Val Glu Val His Val Trp Thr Ile Arg Lys  
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Gly Ile Leu Gln His Phe His Ile Glu Lys Ile Ser Lys Arg Met Phe  
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Glu Glu Leu Pro His Phe Lys Leu Val Thr Arg Thr Thr Leu Ser Gln  
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Trp Lys Ile Phe Thr Glu Gly Glu Ala Gln Ile Ser Gln Met Cys Ser  
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Leu Glu Arg Ser Glu Lys Gly His Cys  
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Glu Gly Val Phe Tyr Val Asn Asp Ala Leu Glu Lys Leu Met Phe Glu
 35           40           45

Glu Leu Arg Asn Ala Cys Arg Gly Gly Gly Val Gly Gly Phe Leu Pro
 50           55           60

Ala Met Lys Gln Ile Gly Asn Val Ala Ala Leu Pro Gly Ile Val His
 65           70           75           80

Arg Ser Ile Gly Leu Pro Asp Val His Ser Gly Tyr Gly Phe Ala Ile
 85           90           95

Gly Asn Met Ala Ala Phe Asp Met Asn Asp Pro Glu Ala Val Val Ser
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Pro Gly Gly Val Gly Phe Asp Ile Asn Cys Gly Val Arg Leu Leu Arg
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Thr Asn Leu Asp Glu Ser Asp Val Gln Pro Val Lys Glu Gln Leu Ala
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Gln Ala Met Phe Asp His Ile Pro Val Gly Val Gly Ser Lys Gly Val
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Ile Pro Met Asn Ala Lys Asp Leu Glu Glu Ala Leu Glu Met Gly Val
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Asp Trp Ser Leu Arg Glu Gly Tyr Ala Trp Ala Glu Asp Lys Glu His
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Cys Glu Glu Tyr Gly Arg Met Leu Gln Ala Asp Pro Asn Lys Val Ser
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Ala Arg Ala Lys Lys Arg Gly Leu Pro Gln Leu Gly Thr Leu Gly Ala
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Gly Asn His Tyr Ala Glu Ile Gln Val Val Asp Glu Ile Phe Asn Glu
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Tyr Ala Ala Lys Lys Met Gly Ile Asp His Lys Gly Gln Val Cys Val
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Met Ile His Ser Gly Ser Arg Gly Leu Gly His Gln Val Ala Thr Asp
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Asn Asp Arg Gln Leu Ala Cys Ala Arg Ile Ala Ser Pro Glu Gly Gln
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 His Asn Ile Ala Lys Val Glu Gln His Val Val Asp Gly Lys Glu Arg  
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 Thr Leu Leu Val His Arg Lys Gly Ser Thr Arg Ala Phe Pro Pro His  
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 His Pro Leu Ile Ala Val Asp Tyr Gln Leu Thr Gly Gln Pro Val Leu  
 385 390 395 400  
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 405 410 415  
 Gln Gly Met Thr Glu Thr Phe Gly Thr Thr Cys His Gly Ala Gly Arg  
 420 425 430  
 Ala Leu Ser Arg Ala Lys Ser Arg Arg Asn Leu Asp Phe Gln Asp Val  
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 450 455 460  
 Lys Leu Val Met Glu Glu Ala Pro Glu Ser Tyr Lys Asn Val Thr Asp  
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 Val Val Asn Thr Cys His Asp Ala Gly Ile Ser Lys Lys Ala Ile Lys  
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<210> 79  
 <211> 1178  
 <212> DNA  
 <213> Homo sapiens

<400> 79  
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 tcaggtaact attttacacc acaacagaca agcagctttc tcaaatectc aactcctcct 240  
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 gtcatggcaa actctgctgg acttaacttc atcaatgtag tgggctctgt ttgtggggcc 420  
 caggctttga tgagtgggtc aaaccccatg ctgggctgta acactgggtg cataactcct 480  
 gcaggaataa acctgagcgg ctttctaccc tcaggaggct tgctacaaa tgcactgccc 540  
 agtgcaatgc aggcagcttc tcaagcaggt gttccatttg gtttaaaaaa tacttcaagt 600  
 ctcaggccct taaatctact ccagcttcca ggtggttcac ttatttttaa cactctgcag 660  
 cagcagcaac agcagctctc ccagtttaca ccacaacaac ctcagcagcc cacaacttgt 720  
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 acacaagagc actgaatcaa aagaattgag tttctacttt ttgttttttt taatgtgtca 1080  
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<210> 80

<211> 310

<212> PRT

<213> Homo sapiens

<400> 80

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 Leu Gly Lys Gly Val Lys His Arg Pro Pro Pro Ile Lys Leu Pro Ser  
 35 40 45  
 Ser Ser Gly Asn Ser Ser Ser Gly Asn Tyr Phe Thr Pro Gln Gln Thr  
 50 55 60  
 Ser Ser Phe Leu Lys Ser Pro Thr Pro Pro Pro Ser Ser Lys Pro Ser  
 65 70 75 80  
 Ser Ile Pro Arg Lys Ser Ser Val Asp Leu Asn Gln Val Ser Met Leu  
 85 90 95  
 Ser Pro Ala Ala Leu Ser Pro Ala Ser Ser Ser Gln Arg Thr Thr Ala  
 100 105 110  
 Thr Gln Val Met Ala Asn Ser Ala Gly Leu Asn Phe Ile Asn Val Val  
 115 120 125  
 Gly Ser Val Cys Gly Ala Gln Ala Leu Met Ser Gly Ser Asn Pro Met  
 130 135 140  
 Leu Gly Cys Asn Thr Gly Ala Ile Thr Pro Ala Gly Ile Asn Leu Ser  
 145 150 155 160  
 Gly Leu Leu Pro Ser Gly Gly Leu Leu Pro Asn Ala Leu Pro Ser Ala  
 165 170 175  
 Met Gln Ala Ala Ser Gln Ala Gly Val Pro Phe Gly Leu Lys Asn Thr  
 180 185 190  
 Ser Ser Leu Arg Pro Leu Asn Leu Leu Gln Leu Pro Gly Gly Ser Leu  
 195 200 205  
 Ile Phe Asn Thr Leu Gln Gln Gln Gln Gln Gln Leu Ser Gln Phe Thr  
 210 215 220  
 Pro Gln Gln Pro Gln Gln Pro Thr Thr Cys Ser Pro Gln Gln Pro Gly  
 225 230 235 240  
 Glu Gln Gly Ser Glu Gln Gly Ser Thr Ser Gln Glu Gln Ala Leu Ser

245 250 255  
 Ala Gln Gln Ala Ala Val Ile Asn Leu Thr Gly Val Gly Ser Phe Met  
 260 265 270  
 Gln Ser Gln Ala Ala Ala Val Ala Ile Leu Ala Ala Ser Asn Gly Tyr  
 275 280 285  
 Gly Ser Ser Ser Ser Thr Asn Ser Ser Ala Thr Ser Ser Ser Ala Tyr  
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 305 310

<210> 81  
 <211> 641  
 <212> DNA  
 <213> Homo sapiens

<400> 81  
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 cttattggty cctgccccag cctaccccag gtgccagcag actctcgtgc acaggaggct 180  
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 aaaaattata ttcccttatat tcttgcttat atcaatgctc tctctgtaaa acctcttcc 300  
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 cctggatggt gtcactagtc tagtggcttt tgctaaataa acctttctta tttctaaaaa 540  
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<210> 82  
 <211> 94  
 <212> PRT  
 <213> Homo sapiens

<400> 82  
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 Trp Thr Pro Gly Val Leu Thr Leu Leu Val Pro Ala Pro Ala Tyr Pro  
 35 40 45  
 Arg Cys Gln Gln Thr Leu Val His Arg Arg Leu Pro Gln Leu Trp Ser  
 50 55 60  
 Gln Glu Arg Ile Ser Leu His Trp Met Asp Cys Ile Leu Arg Leu Lys  
 65 70 75 80  
 Ile Ile Phe Leu Ile Phe Leu Leu Ile Ser Met Leu Ser Leu  
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<210> 83  
 <211> 832

<212> DNA  
 <213> Homo sapiens

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 <211> 144  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Asp His His Cys Val Trp Val Asn Asn Cys Ile Gly Ala Trp Asn Ile  
 35 40 45  
 Arg Tyr Phe Leu Ile Tyr Val Leu Thr Leu Thr Ala Ser Ala Ala Thr  
 50 55 60  
 Val Ala Ile Val Ser Thr Thr Phe Leu Val His Leu Val Val Met Ser  
 65 70 75 80  
 Asp Leu Tyr Gln Glu Thr Tyr Ile Asp Asp Leu Gly His Leu Pro Cys  
 85 90 95  
 Tyr Gly His Gly Leu Ser Tyr Ser Val Pro Val Pro Asp Phe Ser Thr  
 100 105 110  
 Asp Cys Leu His Ala Gly Leu Cys Arg Gly Ser Glu Leu Pro Pro Gly  
 115 120 125  
 Trp Leu Pro Val Val Cys Pro Val Ser Gly Gly His Gln Pro Asp Tyr  
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<210> 85  
 <211> 3790  
 <212> DNA  
 <213> Homo sapiens

<400> 85  
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 tacatgcatg cttacctaac agtttgaaat agtattgatc tactgctggt aaaaaaaaaa 3780  
 aaaaaaaaaa 3790

<210> 86  
 <211> 940  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
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 20 25 30  
 Leu Arg Leu Ser Phe Ser Glu Ile Asn Thr Arg Val Ile Lys Glu Asp  
 35 40 45  
 Ile Val Arg Arg Glu Arg Ile Gly Phe Arg Val Gln Pro Asp Gln Gly  
 50 55 60  
 Lys Ile Phe Tyr Ser Ser Ile Lys Glu Met Lys Pro Pro Leu Arg Gly  
 65 70 75 80  
 His Gly Lys Gly Ala Trp Gly Lys Glu Asn Val Arg Lys Thr Glu Glu  
 85 90 95  
 Ser Val Leu Lys Val Glu Val Asp Leu Asp Gln Thr Gln Arg Glu Arg  
 100 105 110  
 Lys Met Gln Asn Ala Leu Gly Arg Gly Lys Val Val Pro Leu Trp His  
 115 120 125  
 Pro Ala His Leu Gln Thr Leu Pro Val Thr Pro Asn Lys Gln Lys Thr  
 130 135 140  
 Asp Gly Arg Gly Thr Lys Pro Glu Ala Ser Ser His Gln Gly Thr Pro  
 145 150 155 160  
 Lys Gln Thr Thr Ala Gln Gly Ala Pro Lys Thr Ser Phe Ile Ala Ala  
 165 170 175  
 Lys Gly Thr Gln Val Val Lys Ile Ser Val His Met Gly Arg Val Ser  
 180 185 190  
 Leu Lys Gln Glu Pro Arg Lys Ser His Ser Pro Ser Ser Asp Thr Ser  
 195 200 205  
 Lys Leu Ala Ala Glu Arg Asp Leu Asn Val Thr Ile Ser Leu Ser Thr  
 210 215 220  
 Asp Arg Pro Lys Gln Arg Ser Gln Ala Val Ala Asn Glu Arg Ala His  
 225 230 235 240  
 Pro Ala Ser Thr Ala Val Pro Lys Ser Gly Glu Ala Met Ala Leu Asn  
 245 250 255  
 Lys Thr Lys Thr Gln Ser Lys Glu Val Asn Ala Asn Lys His Lys Ala  
 260 265 270



Cys Asn Val Gly Trp Leu Glu Pro Leu Leu Glu Arg Val Tyr Leu Ser  
595 600 605

Arg Lys Lys Val Ala Cys Pro Val Ile Glu Val Ile Asn Asp Lys Asp  
610 615 620

Met Ser Tyr Met Thr Val Asp Asn Phe Gln Arg Gly Ile Phe Val Trp  
625 630 635 640

Pro Met Asn Phe Gly Trp Arg Thr Ile Pro Pro Asp Val Ile Ala Lys  
645 650 655

Asn Arg Ile Lys Glu Thr Asp Thr Ile Arg Cys Pro Val Met Ala Gly  
660 665 670

Gly Leu Phe Ser Ile Asp Lys Ser Tyr Phe Phe Glu Leu Gly Thr Tyr  
675 680 685

Asp Pro Gly Leu Asp Val Trp Gly Gly Glu Asn Met Glu Leu Ser Phe  
690 695 700

Lys Val Trp Met Cys Gly Gly Glu Ile Glu Ile Ile Pro Cys Ser Arg  
705 710 715 720

Val Gly His Ile Phe Arg Asn Asp Asn Pro Tyr Ser Phe Pro Lys Asp  
725 730 735

Arg Met Lys Thr Val Glu Arg Asn Leu Val Arg Val Ala Glu Val Trp  
740 745 750

Leu Asp Glu Tyr Lys Glu Leu Phe Tyr Gly His Gly Asp His Leu Ile  
755 760 765

Asp Gln Gly Leu Asp Val Gly Asn Leu Thr Gln Gln Arg Glu Leu Arg  
770 775 780

Lys Lys Leu Lys Cys Lys Ser Phe Lys Trp Tyr Leu Glu Asn Val Phe  
785 790 795 800

Pro Asp Leu Arg Ala Pro Ile Val Arg Ala Ser Gly Val Leu Ile Asn  
805 810 815

Val Ala Leu Gly Lys Cys Ile Ser Ile Glu Asn Thr Thr Val Ile Leu  
820 825 830

Glu Asp Cys Asp Gly Ser Lys Glu Leu Gln Gln Phe Asn Tyr Thr Trp  
835 840 845

Leu Arg Leu Ile Lys Cys Gly Glu Trp Cys Ile Ala Pro Ile Pro Asp  
850 855 860

Lys Gly Ala Val Arg Leu His Pro Cys Asp Asn Arg Asn Lys Gly Leu  
865 870 875 880

Lys Trp Leu His Lys Ser Thr Ser Val Phe His Pro Glu Leu Val Asn  
885 890 895

His Ile Val Phe Glu Asn Asn Gln Gln Leu Leu Cys Leu Glu Gly Asn  
900 905 910



Phe Ser Gln Lys Ile Leu Lys Val Ala Ala Cys Asp Pro Val Lys Pro  
 915 920 925

Tyr Gln Lys Trp Lys Phe Glu Lys Tyr Tyr Glu Ala  
 930 935 940

<210> 87  
 <211> 1200  
 <212> DNA  
 <213> Homo sapiens

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 actcttttga gatgccatt ctacttttga atttagcttt tactaattcg catctggaag 1080  
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<210> 88  
 <211> 286  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
 Met Ser Tyr Ile Pro Gly Gln Pro Val Thr Ala Val Val Gln Arg Val  
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 Glu Ile His Lys Leu Arg Gln Gly Glu Asn Leu Ile Leu Gly Phe Ser  
 20 25 30  
 Ile Gly Gly Gly Ile Asp Gln Asp Pro Ser Gln Asn Pro Phe Tyr Glu  
 35 40 45  
 Asp Lys Thr Asp Lys Gly Ile Tyr Val Thr Arg Val Ser Glu Gly Gly  
 50 55 60  
 Pro Ala Glu Ile Ala Gly Leu Gln Ile Gly Asp Lys Ile Met Gln Val  
 65 70 75 80  
 Asn Gly Trp Asp Met Thr Met Val Thr His Asp Gln Ala Arg Lys Arg  
 85 90 95  
 Leu Thr Lys Arg Ser Glu Glu Val Val Arg Leu Leu Val Thr Arg Gln



<210> 90  
 <211> 149  
 <212> PRT  
 <213> Homo sapiens

<400> 90  
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 1 5 10 15  
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 20 25 30  
 Val Tyr Ala Leu Val Val Val Ser Tyr Phe Leu Ile Thr Gly Gly Ile  
 35 40 45  
 Ile Tyr Asp Val Ile Val Glu Pro Pro Ser Val Gly Ser Met Thr Asp  
 50 55 60  
 Glu His Gly His Gln Arg Pro Val Ala Phe Leu Ala Tyr Arg Val Asn  
 65 70 75 80  
 Gly Gln Tyr Ile Met Glu Gly Leu Ala Ser Ser Phe Leu Phe Thr Met  
 85 90 95  
 Gly Gly Leu Gly Phe Ile Ile Leu Asp Arg Ser Asn Ala Pro Asn Ile  
 100 105 110  
 Pro Lys Leu Asn Arg Phe Leu Leu Leu Phe Ile Gly Phe Val Cys Val  
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 Gly Tyr Leu Met Gly  
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<210> 91  
 <211> 3901  
 <212> DNA  
 <213> Homo sapiens

<400> 91  
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 <212> PRT  
 <213> Homo sapiens

<400> 92  
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 Asn Thr Leu Lys Phe Ser Thr Thr Ser Leu Cys Cys Leu Val Gly Phe  
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 <211> 2203  
 <212> DNA  
 <213> Homo sapiens

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 <212> PRT

<213> Homo sapiens

<400> 94

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Lys Val His Leu Asp Ser Ala Val Ala Leu Ala Ala Glu Ser Pro Val  
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Asn Met Met Pro Trp Gln Gly Asp Thr Asn Asn Met Ile Asp Arg Phe  
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Asp Val Arg Ala His Leu Asp His Ile Pro Asp Tyr Thr Pro Pro Leu  
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Leu Thr Thr Ile Ser Pro Glu Gln Glu Ser Asp Glu Arg Lys Cys Asn  
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Tyr Glu Arg Tyr Arg Gly Leu Val Gln Asn Asp Phe Ala Gly Ile Ser  
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Glu Glu Gln Cys Leu Tyr Gln Ile Tyr Ile Asp Glu Leu Tyr Gly Gly  
130 135 140  
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Ala Ser Ile Gly Tyr Thr Tyr Glu Asp Ser Thr Val Ala Glu Val Glu  
165 170 175  
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Ser Asn Ser Asp Glu Asp Glu Val Ile Pro Asp Ile Asp Val Glu Val  
195 200 205  
Asp Val Asp Glu Leu Asn Gln Glu Gln Val Ala Asp Leu Asn Lys Gln  
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Ala Thr Thr Tyr Gly Met Ala Asp Gly Asp Phe Val Arg Met Leu Arg  
225 230 235 240  
Lys Asp Lys Glu Glu Ala Glu Ala Ile Lys His Ala Lys Ala Leu Glu  
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Glu Phe Arg Glu Lys Arg Leu Arg Gly Arg Lys Ile Ser Pro Pro Ser  
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 Thr Gly Lys Pro Pro Ala Pro Pro Gln Pro Gly Gly Pro Ala Pro Gly  
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 Asp Gly His Arg Tyr Ser Arg Ser Pro Ala Arg Arg Gly Gly Tyr Gly  
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 Ser Trp Ser Leu Ser Pro Ser Arg Ser Arg Ser Leu Thr Arg Ser Arg  
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 Ser His Ser Pro Ser Pro Ser Gln Ser Arg Ser Arg Ser Arg Ser Arg  
 515 520 525  
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 545 550 555 560  
 Ala Gly Lys Glu Thr Gly Ala Ala Lys Pro Lys Leu Thr Pro Gln Glu  
 565 570 575  
 Lys Leu Lys Leu Arg Met Gln Lys Ala Leu Asn Arg Gln Phe Lys Ala  
 580 585 590  
 Asp Lys Lys Ala Ala Gln Glu Lys Met Ile Gln Gln Glu His Glu Arg  
 595 600 605  
 Gln Glu Arg Glu Asp Glu Leu Arg Ala Met Ala Arg Lys Ile Arg Met  
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Lys Glu Arg Glu Arg Arg Glu Lys Glu Arg Glu Glu Trp Glu Arg Gln  
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<212> DNA  
<213> Homo sapiens

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<211> 204  
<212> PRT  
<213> Homo sapiens

<400> 96  
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Ser Phe Ile Lys Trp Cys Asn Ser Gly Ser Gln Glu Glu Gly Tyr Ser  
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Gln Tyr Gln Arg Met Leu Ser Thr Leu Ser Gln Cys Glu Phe Ser Met  
50 55 60  
Gly Lys Thr Leu Leu Val Tyr Asp Met Asn Leu Arg Glu Met Glu Asn  
65 70 75 80  
Tyr Glu Lys Ile Tyr Lys Glu Ile Glu Cys Ser Ile Ala Gly Ala His  
85 90 95

Glu Lys Ile Ala Glu Cys Lys Lys Gln Ile Leu Gln Ala Lys Arg Ile  
100 105 110

Arg Lys Asn Arg Gln Glu Tyr Asp Ala Leu Ala Lys Val Ile Gln His  
115 120 125

His Pro Asp Arg His Glu Thr Leu Lys Glu Leu Glu Ala Leu Gly Lys  
130 135 140

Glu Leu Glu His Leu Ser His Ile Lys Glu Ser Val Glu Asp Lys Leu  
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Glu Leu Arg Arg Lys Gln Phe His Val Leu Leu Ser Thr Ile His Glu  
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Leu Gln Gln Thr Leu Glu Asn Asp Glu Lys Leu Ser Glu Val Glu Glu  
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<211> 97  
<212> PRT  
<213> Homo sapiens

<400> 98  
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Asp Ile Glu Glu Lys Lys Ser Ile Lys Lys Lys Ile Lys Glu Leu Lys  
35 40 45

Phe Leu Asp Ser Lys Ile Ala Gln Asn Leu Cys Lys Tyr His Ile Pro  
50 55 60

Ile Pro Phe Lys Asp Ser Gly Asn Ile Ser Leu Asn Asp Phe Ile Phe  
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Phe Lys Thr Asp Tyr Ser Leu Phe Ala Ile Phe Ile Leu Leu Leu Tyr  
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Ala

<210> 99  
<211> 1375  
<212> DNA  
<213> Homo sapiens

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<211> 132  
<212> PRT  
<213> Homo sapiens

<400> 100  
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Cys Arg Gly Ser Trp Gln Leu Leu Gly Glu Val Ser Trp His Arg Leu  
35 40 45  
Thr Leu Leu Ser Gly Thr Thr Ser Phe Pro Phe Glu Glu Thr Ala Thr

50 55 60

Ala Val Ala Lys Ala Ala Ala Pro Ala Met Arg Val Tyr Ile Phe  
65 70 75 80

Phe Thr Gln Ser Ser Gly Ile Val His Leu Phe Phe Lys Thr Gln Arg  
85 90 95

Gly Lys Glu Pro Cys Ile Ile Cys Glu His Cys Ile Ile Gly Asn Val  
100 105 110

Val Gln Thr Leu Leu Tyr Ser Asp Leu Ser Cys Ser Cys Ser Lys Asn  
115 120 125

Pro Leu Trp Thr  
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<210> 101  
<211> 1213  
<212> DNA  
<213> Homo sapiens

<400> 101

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Leu Cys Gln Val Val Glu Leu Gly Pro Ser Pro Tyr Leu Ser Leu Val  
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<213> Homo sapiens

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Tyr Glu Phe Glu Ile Thr Asp Leu Phe Ser Ser Tyr Cys Ile His Ile  
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Asn Ile Cys Glu Phe Val Val Gln Leu Phe Ile Gln Thr Lys Asn Ile  
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Pro Ser Arg Lys Leu His Phe Tyr His Lys His Phe Asn Ile Thr Asn  
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<212> PRT  
<213> Homo sapiens

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35 40 45

Ser Ser Ser Ser Thr Asp Glu Ser Glu Asp Glu Lys Glu Glu Lys Leu  
50 55 60

Thr Asp Gln Ser Arg Ser Lys Leu Tyr Asp Glu Glu Ser Leu Leu Ser  
65 70 75 80

Leu Thr Met Ser Gln Asp Gly Phe Pro Asn Glu Asp Gly Glu Gln Met  
85 90 95

Thr Pro Glu Leu Leu Leu Leu Gln Glu Arg Gln Arg Ala Ser Glu Trp  
100 105 110

Pro Lys Asp Arg Val Leu Ile Asn Arg Ile Asp Leu Val Cys Gln Ala  
115 120 125

Val Leu Ser Gly Lys Trp Pro Ser Ser Arg Arg Ser Gln Glu Met Val  
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Leu Thr Pro Gly Glu Tyr Gly Asp Ser Pro Val Pro Thr Pro Arg Ser  
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Lys His Lys Leu Met Ala Asn Gly Val Met Gly Asp Gly His Pro Leu  
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 Pro Gly Asp Phe Asp Tyr Leu Gly Pro Ser Ala Ser Ser Gln Met Ser



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<212> DNA  
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<210> 112  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 112  
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 Leu Ser Leu Tyr Thr His Val Thr Cys Ser Ser Leu Pro Ser Ser Leu  
                     20                    25                    30  
 Cys Leu Tyr Ile Tyr Tyr Tyr His Arg Gly Leu Gly Lys Lys Thr Pro  
                     35                    40                    45  
 Thr Ala Ala Pro His Thr His Pro Pro Ala Leu Tyr His Leu Leu Cys  
                     50                    55                    60  
 Phe Val Phe Leu Cys Arg Ile His Asp Phe Leu Lys Tyr Asn Phe Phe  
                     65                    70                    75                    80  
 Asn Val Tyr Ile Leu Tyr Ala Phe Ser His Ser Tyr Val Lys Ser Gly  
                     85                    90                    95

Arg His Arg Leu Val Phe Leu Phe Thr Val Asp Ala Ser Val Pro Lys  
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Ile Cys Ile Ala  
 115

<210> 113  
 <211> 2759  
 <212> DNA  
 <213> Homo sapiens

<400> 113  
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 gccgctgcc acaggctagg cctgcctgca gccaaagagg ctgctcaaac tctagatgcc 180  
 atttgaggac atgaggacct gagccagag gtggcagtgt cctaccagg gaagtcaaca 240  
 gatcgtgctc caggtcccag ctctgggctg ggccaggact aaatcctggc tcccccttct 300  
 tggactaag gggattagt cttggttgc tgtaggggt cagagtaggg agggttccag 360  
 gaagggttcc agagtgggt cacaggggac ctctccccct ggctcttgg agtccaggtc 420  
 gtcgagggcg caaagctgca cgccatcctg ggcaagctgg gcccgcagcg tgggcgcggt 480  
 gaggacgcgc agctcatgca gccgctccca agagcaagag aaagcgtcgg ggccttcacc 540  
 gcagcgccg gtgggagga cactgggtga gccgggtgc gccatcagct cggctgtcag 600  
 ggtgtggccc gctagggtac ctccaggac ccgcgccagg gcccggaca cgcggtgagc 660  
 ggacatgtgc cggccgcaag tgctcaggcc cacgaaggcg tctgtccacc gcaggccgtg 720  
 gcgggagaag ggcccacggc ggcccggcg tcgcgtcca cggcgcaggc gaaggcacgc 780  
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 agttgggcct cgagctcctc ccgcacctag agggcgagcg agagacacct tgagcgaccg 1020  
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 cggaagtcat ccaccgccag ctcttaacgg cctcacagta cctccgggc ggagctctgg 1140  
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 cagatccggg tcttgtggct aagagtgcg tggctactcg aatcaaaaca gaggaggggg 1560  
 aggaagccgg cggccagaaa cggcagtgcc agcagcgtcc ggagcagcc cagccttctg 1620  
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<210> 114  
 <211> 99  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 114  
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 His Ala Met Arg Arg Leu Ile Asn Leu Leu Arg Gln Ser Gln Ser Tyr  
           20                  25                  30  
  
 Cys Thr Asp Thr Glu Cys Leu Gln Glu Leu Pro Gly Pro Ser Gly Asp  
           35                  40                  45  
  
 Asn Gly Ile Ser Val Thr Met Ile Leu Val Ala Trp Met Val Ile Ala  
   50                  55                  60  
  
 Leu Ile Leu Phe Leu Leu Arg Pro Pro Asn Leu Arg Gly Ser Ser Leu  
   65                  70                  75                  80  
  
 Pro Gly Lys Pro Thr Ser Pro His Asn Gly Gln Asp Pro Pro Ala Pro  
           85                  90                  95  
  
 Pro Val Asp

<210> 115  
 <211> 1404  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
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 gcctctgttc tcggaatccg ggtgctgcgg attgaggtcc cggttcctaa cggtgggatc 180  
 ggtgtcctcg ggatgagatt tggcgtttcc tcggggcctt ggtgggatcg gtgtcctcag 240  
 gatgagattt agggtttccct cggggccttc gggatcttca cctaataatcc ggtattattt 300  
 tatgagagga gtggtcttgg ctgtcagaac tggatccctg gggtgatatt tgggaattag 360  
 tggagtgatc tctgaagacc tagggctatg atctggagct gctgtggctg aaatttgggg 420  
 cctctgaagt ggcatggaga ttgaggtcca gagagcctga gatcttgagg gctgacattt 480  
 ggagagatgg ggtcaggggt tgtctttggg ccttgactgc tttgggcctt tctcactctc 540  
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 gctcacaggg tctgaaggcc acgcatgagg caaaggtaaa gttctgagcc acccggtgcc 660  
 tccttcccag gactgcaaga tggaggaagg cgggaacctt ggaggcctga ttaagatggt 720  
 ccactactcg gtcttgtcag gtgcctgggg catgcaaag tgggtgacct tcgtctcagg 780  
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 gctggccttg ccctggaaat aaggagcctc tagcatgggc cctgcatgct aataaatgct 1380  
 tcttcagaaa aaaaaaaaaa aaaa 1404



<210> 116  
 <211> 184  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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 Ser Ala Leu Thr Pro Leu Trp Ser Pro Tyr Pro Ala Gly Phe Leu Leu  
 20 25 30  
 Phe Arg Ser Leu Pro Arg His Thr Phe Gly Leu Val Gln Ser Lys Leu  
 35 40 45  
 Phe Pro Phe Tyr Phe His Ile Ser Met Gly Cys Ala Phe Ile Asn Leu  
 50 55 60  
 Cys Ile Leu Ala Ser Gln His Ala Trp Ala Gln Leu Thr Phe Trp Glu  
 65 70 75 80  
 Ala Ser Gln Leu Tyr Leu Leu Phe Leu Ser Leu Thr Leu Ala Thr Val  
 85 90 95  
 Asn Ala Arg Trp Leu Glu Pro Arg Thr Thr Ala Ala Met Trp Ala Leu  
 100 105 110  
 Gln Thr Val Glu Lys Glu Arg Gly Leu Gly Gly Glu Val Pro Gly Ser  
 115 120 125  
 His Gln Gly Pro Asp Pro Tyr Arg Gln Leu Arg Glu Lys Asp Pro Lys  
 130 135 140  
 Tyr Ser Ala Leu Arg Gln Asn Phe Phe Arg Tyr His Gly Leu Ser Ser  
 145 150 155 160  
 Leu Cys Asn Leu Gly Cys Val Leu Ser Asn Gly Leu Cys Leu Ala Gly  
 165 170 175  
 Leu Ala Leu Glu Ile Arg Ser Leu  
 180

<210> 117  
 <211> 1801  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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 tgaatagctt taattcagct gttgaatctc acttgaattt gagcaaaacc ttcattcttta 180  
 tatgtatctg gacaaattac ttcaattgct tgacagtaat gaccaatcaa tttattttaaa 240  
 atagtatcat ttagtaggac agtgtttttc tctggtttga gcaacgaatt caaccagtcc 300  
 tctgggttga tcatcatcat catcatcatt tggttatcag ttcttgagtt atttttacca 360  
 gggagttttaa taccttttaga caactatttt gaattatctc aggaatgtca tatatctctg 420  
 cctcttttaga gtcagtcact ggcactttgt ctgttttggtg acatcatggt tccctgactg 480  
 ttcttcatct ttgtagttat acattgatat ctgtgcattg aatatgtagg tatttataaa 540  
 cagtctttgc aatctggctt tgtctgtgat tgccttgta tagtaggtct gtccagaaat 600  
 tgaagcata ctgtcttttt tggctcttaa gcccgtaac gctacagccc gtgtagtgcc 660

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aaatggtgcc ctaagcccag gtccctgca gtccactctg tgatttggtt gttgactgct 720
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ttgatagata cagtatgata gaaaaagatc aggaaggat atgctgacat ttaaactctgg 1680
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<210> 118
<211> 86
<212> PRT
<213> Homo sapiens

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Glu Thr Asp Ser Arg Glu Ile Leu Gln Val Arg Cys Tyr Val Gly Leu
      20             25             30

Arg Glu Arg Cys Tyr Asp Gln Thr Glu Pro Phe Ser Leu Pro Ser Val
      35             40             45

His Gly Phe Ser Trp Leu Cys Gly Pro Val Ser Cys His Ser Phe Thr
      50             55             60

Pro Asn Phe Trp Asp Ile Gln Gly Asn Asn Leu Ala Thr Gly Tyr Leu
      65             70             75             80

Leu Val Glu Ile Met Trp
              85

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<210> 119
<211> 29
<212> DNA
<213> Artificial Sequence

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<220>
<223> oligonucleotide

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<220>
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<222> (2)
<223> biotinylated phosphoramidite residue

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<400> 119

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ancgggagcc tcctgacat ctctcttc

29

<210> 120

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

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<222> (2)

<223> biotinylated phosphoramidite residue

<400> 120

cncacagaaa attcaataag accctcgct

29

<210> 121

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoramidite residue

<400> 121

cncagctctt cgtagggaag ttctgactt

29

<210> 122

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

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<222> (2)

<223> biotinylated phosphoramidite residue

<400> 122

antcctgcac accagccagt aacgccacc

29

<210> 123

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

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<222> (2)  
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<400> 123  
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<210> 124  
 <211> 29  
 <212> DNA  
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<220>  
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<220>  
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<400> 124  
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<210> 125  
 <211> 29  
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<220>  
 <223> oligonucleotide

<220>  
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<400> 125  
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<210> 126  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
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<220>  
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 <222> (2)  
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<400> 126  
 gngttttcgg tgtcgtggt gtagaggat 29

<210> 127  
 <211> 29  
 <212> DNA  
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<220>

<223> oligonucleotide

<220>  
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<400> 127  
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<210> 128  
 <211> 29  
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<220>  
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<400> 128  
 anactgaaaa ctgagtatgt gcgagtgtgta 29

<210> 129  
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<400> 129  
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<210> 131  
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<212> DNA  
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<220>  
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<220>  
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<222> (2)  
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<400> 131  
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29

<210> 132  
<211> 29  
<212> DNA  
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<220>  
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<220>  
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<222> (2)  
<223> biotinylated phosphoramidite residue

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29

<210> 133  
<211> 29  
<212> DNA  
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<220>  
<223> oligonucleotide

<220>  
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<222> (2)  
<223> biotinylated phosphoramidite residue

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29

<210> 134  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> oligonucleotide

<220>  
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<222> (2)  
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<400> 134

gngcactgta ttgagctgat tgctgaagc

29

<210> 135

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoaramidite residue

<400> 135

cncagaagca gaagaatgac aggcaacac

29

<210> 136

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoaramidite residue

<400> 136

anacattctg agtagttgca tgatttccc

29

<210> 137

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

<220>

<221> misc\_feature

<222> (2)

<223> biotinylated phosphoaramidite residue

<400> 137

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29

<210> 138

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> oligonucleotide

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<222> (2)  
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gntgacttca atctcctcac cttccaccg

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<400> 151

gngggatgag gcaatgaaca caatgaaag

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<210> 152

<211> 29

<212> DNA

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<400> 152

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29

<210> 153

<211> 29

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<400> 157

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<400> 158

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<210> 159

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<400> 159

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<223> biotinylated phosphoramidite residue

<400> 160

anctgccatg tcaaagagga gccagatga

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<210> 161

<211> 29

<212> DNA

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<211> 20

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<400> 166

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<210> 167

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<400> 167

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<210> 168

<211> 29

<212> DNA

<213> Artificial Sequence

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<222> (2)

<223> biotinylated phosphoramidite residue

<400> 168

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<210> 169

<211> 29

<212> DNA

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<400> 175  
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<210> 176  
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<212> DNA  
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<211> 388  
<212> PRT  
<213> Homo sapiens

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Arg Arg Ser Ala Met Leu Cys Ile Leu Thr Val Pro Ala Ala Met Thr  
20 25 30  
Ser His Asp Leu Met Lys Phe Val Ala Pro Phe Asn Glu Val Ile Glu  
35 40 45  
Gln Met Lys Ile Ile Arg Asp Ser Thr Pro Asn Gln Tyr Met Val Leu  
50 55 60  
Ile Lys Phe Arg Ala Gln Ala Asp Ala Asp Ser Phe Tyr Met Thr Cys  
65 70 75 80  
Asn Gly Arg Gln Phe Asn Ser Ile Glu Asp Asp Val Cys Gln Leu Val  
85 90 95  
Tyr Val Glu Arg Ala Glu Val Leu Lys Ser Glu Asp Gly Ala Ser Leu  
100 105 110  
Pro Val Met Asp Leu Thr Glu Leu Pro Lys Cys Thr Val Cys Leu Glu  
115 120 125  
Arg Met Asp Glu Ser Val Asn Gly Ile Leu Thr Thr Leu Cys Asn His  
130 135 140  
Ser Phe His Ser Gln Cys Leu Gln Arg Trp Asp Asp Thr Thr Cys Pro  
145 150 155 160  
Val Cys Arg Tyr Cys Gln Thr Pro Glu Pro Val Glu Glu Asn Lys Cys  
165 170 175  
Phe Glu Cys Gly Val Gln Glu Asn Leu Trp Ile Cys Leu Ile Cys Gly  
180 185 190  
His Ile Gly Cys Gly Arg Tyr Val Ser Arg His Ala Tyr Lys His Phe  
195 200 205  
Glu Glu Thr Gln His Thr Tyr Ala Met Gln Leu Thr Asn His Arg Val  
210 215 220  
Trp Asp Tyr Ala Gly Asp Asn Tyr Val His Arg Leu Val Ala Ser Lys  
225 230 235 240  
Thr Asp Gly Lys Ile Val Gln Tyr Glu Cys Glu Gly Asp Thr Cys Gln  
245 250 255  
Glu Glu Lys Ile Asp Ala Leu Gln Leu Glu Tyr Ser Tyr Leu Leu Thr  
260 265 270

Ser Gln Leu Glu Ser Gln Arg Ile Tyr Trp Glu Asn Lys Ile Val Arg  
275 280 285

Ile Glu Lys Asp Thr Ala Glu Glu Ile Asn Asn Met Lys Thr Lys Phe  
290 295 300

Lys Glu Thr Ile Glu Lys Cys Asp Asn Leu Glu His Lys Leu Asn Asp  
305 310 315 320

Leu Leu Lys Glu Lys Gln Ser Val Glu Arg Lys Cys Thr Gln Leu Asn  
325 330 335

Thr Lys Val Ala Lys Leu Thr Asn Glu Leu Lys Glu Glu Gln Glu Met  
340 345 350

Asn Lys Cys Leu Arg Ala Asn Gln Val Leu Leu Gln Asn Lys Leu Lys  
355 360 365

Glu Glu Glu Arg Val Leu Lys Glu Thr Cys Asp Gln Lys Asp Leu Gln  
370 375 380

Ile Thr Glu Ile  
385

<210> 178  
<211> 171  
<212> PRT  
<213> Homo sapiens

<400> 178  
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Ile Ser Met Arg Cys Met Val Gln Phe Val Gly Arg Glu Ala Lys Tyr  
20 25 30

Ser Gly Val Leu Ser Ser Ile Gly Lys Ile Phe Lys Glu Glu Gly Leu  
35 40 45

Leu Gly Phe Phe Val Gly Leu Ile Pro His Leu Leu Gly Asp Val Val  
50 55 60

Phe Leu Trp Gly Cys Asn Leu Leu Ala His Phe Ile Asn Ala Tyr Leu  
65 70 75 80

Val Asp Asp Ser Phe Ser Gln Ala Leu Ala Ile Arg Ser Tyr Thr Lys  
85 90 95

Phe Val Met Gly Ile Ala Val Ser Met Leu Thr Tyr Pro Phe Leu Leu  
100 105 110

Val Gly Asp Leu Met Ala Val Asn Asn Cys Gly Leu Gln Ala Gly Leu  
115 120 125

Pro Pro Tyr Ser Pro Val Phe Lys Ser Trp Ile His Cys Trp Lys Tyr  
130 135 140

Leu Ser Val Gln Gly Gln Leu Phe Arg Gly Ser Ser Leu Leu Phe Arg

[illegible]

Leu Ala

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